

SEQUENCE LISTING

(1) GENERAL INFORMATION

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(ii) TITLE OF THE INVENTION: RANDOM PEPTIDES THAT BIND TO GASTRO-INTESTINAL TRACT (GIT) TRANSPORT RECEPTORS AND RELATED METHODS

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(iii) NUMBER OF SEQUENCES: 407

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: DOS
- (D) SOFTWARE: FastSEQ Version 2.0

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 09/079,678
- (B) FILING DATE: May 15, 1998
- (C) CLASSIFICATION:

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(viii) ATTORNEY/AGENT INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

30

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Arg Ser Gly Ala Tyr Glu Ser Pro Asp Gly Arg Gly Gly Arg Ser Tyr
1 5 10 15
Val Gly Gly Gly Gly Cys Gly Asn Ile Gly Arg Lys His Asn Leu
20 25 30
Trp Gly Leu Arg Thr Ala Ser Pro Ala Cys Trp Asp
35 40

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ser Pro Arg Ser Phe Trp Pro Val Val Ser Arg His Glu Ser Phe Gly
1 5 10 15
Ile Ser Asn Tyr Leu Gly Cys Gly Tyr Arg Thr Cys Ile Ser Gly Thr
20 25 30
Met Thr Lys Ser Ser Pro Ile Tyr Pro Arg His Ser
35 40

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ser Ser Ser Ser Asp Trp Gly Gly Val Pro Gly Lys Val Val Arg Glu
1 5 10 15
Arg Phe Lys Gly Arg Gly Cys Gly Ile Ser Ile Thr Ser Val Leu Thr
20 25 30
Gly Lys Pro Asn Pro Cys Pro Glu Pro Lys Ala Ala
35 40

(2) INFORMATION FOR SEQ ID NO:4:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

30

Arg Val Gly Gln Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala Arg
1 5 10 15

Ser Cys Ala His Gln Gly Cys Gly Ala Gly Thr Arg Asn Ser His Gly
20 25 30
Cys Ile Thr Arg Pro Leu Arg Gln Ala Ser Ala His
35 40

(2) INFORMATION FOR SEQ ID NO:5:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

10 Ser His Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val Phe Arg Glu
1 5 10 15
Leu Arg Asp Arg Trp Asn Ala Thr Ser His His Thr Arg Pro Thr Pro
20 25 30
Gln Leu Pro Arg Gly Pro Asn
35

(2) INFORMATION FOR SEQ ID NO:6:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

20 Ser Pro Cys Gly Gly Ser Trp Gly Arg Phe Met Gln Gly Gly Leu Phe
1 5 10 15
Gly Gly Arg Thr Asp Gly Cys Gly Ala His Arg Asn Arg Thr Ser Ala
20 25 30
Ser Leu Glu Pro Pro Ser Ser Asp Tyr
35 40

(2) INFORMATION FOR SEQ ID NO:7:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

30 Arg Gly Ala Ala Asp Gln Arg Arg Gly Trp Ser Glu Asn Leu Gly Leu
1 5 10 15
Pro Arg Val Gly Trp Asp Ala Ile Ala His Asn Ser Tyr Thr Phe Thr
20 25 30
Ser Arg Arg Pro Arg Pro Pro
35

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

5 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Gly Gly Glu Val Ser Ser Trp Gly Arg Val Asn Asp Leu Cys Ala
1 5 10 15
Arg Val Ser Trp Thr Gly Cys Gly Thr Ala Arg Ser Ala Arg Thr Asp
20 25 30
Asn Lys Gly Phe Leu Pro Lys His Ser Ser Leu Arg
35 40

10 (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ser Asp Ser Asp Gly Asp His Tyr Gly Leu Arg Gly Gly Val Arg Cys
1 5 10 15
Ser Leu Arg Asp Arg Gly Cys Gly Leu Ala Leu Ser Thr Val His Ala
20 25 30
Gly Pro Pro Ser Phe Tyr Pro Lys Leu Ser Ser Pro
35 40

20 (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Arg Ser Leu Gly Asn Tyr Gly Val Thr Gly Thr Val Asp Val Thr Val
1 5 10 15
Leu Pro Met Pro Gly His Ala Asn His Leu Gly Val Ser Ser Ala Ser
20 25 30
Ser Ser Asp Pro Pro Arg Arg
35

(2) INFORMATION FOR SEQ ID NO:11:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

5 Arg Thr Thr Ala Lys Gly Cys Leu Leu Gly Ser Phe Gly Val Leu
1 5 10 15
Ser Gly Cys Ser Phe Thr Pro Thr Ser Pro Pro Pro His Leu Gly Tyr
20 25 30
Pro Pro His Ser Val Asn
35

(2) INFORMATION FOR SEQ ID NO:12:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

15 Ser Pro Lys Leu Ser Ser Val Gly Val Met Thr Lys Val Thr Glu Leu
1 5 10 15
Pro Thr Glu Gly Pro Asn Ala Ile Ser Ile Pro Ile Ser Ala Thr Leu
20 25 30
Gly Pro Arg Asn Pro Leu Arg
35

(2) INFORMATION FOR SEQ ID NO:13:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

25 Arg Trp Cys Gly Ala Glu Leu Cys Asn Ser Val Thr Lys Lys Phe Arg
1 5 10 15
Pro Gly Trp Arg Asp His Ala Asn Pro Ser Thr His His Arg Thr Pro
20 25 30
Pro Pro Ser Gln Ser Ser Pro
35

(2) INFORMATION FOR SEQ ID NO:14:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Arg Trp Cys Gly Ala Asp Asp Pro Cys Gly Ala Ser Arg Trp Arg Gly
1 5 10 15
Gly Asn Ser Leu Phe Gly Cys Gly Leu Arg Cys Ser Ala Ala Gln Ser
20 25 30
5 Thr Pro Ser Gly Arg Ile His Ser Thr Ser Thr Ser
35 40

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

10 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ser Lys Ser Gly Glu Gly Gly Asp Ser Ser Arg Gly Glu Thr Gly Trp
1 5 10 15
Ala Arg Val Arg Ser His Ala Met Thr Ala Gly Arg Phe Arg Trp Tyr
20 25 30
Asn Gln Leu Pro Ser Asp Arg
35

15 (2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

20 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Arg Ser Ser Ala Asn Asn Cys Glu Trp Lys Ser Asp Trp Met Arg Arg
1 5 10 15
Ala Cys Ile Ala Arg Tyr Ala Asn Ser Ser Gly Pro Ala Arg Ala Val
20 25 30
Asp Thr Lys Ala Ala Pro
35

25 (2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Ser Lys Trp Ser Trp Ser Ser Arg Trp Gly Ser Pro Gln Asp Lys Val
1 5 10 15
Glu Lys Thr Arg Ala Gly Cys Gly Gly Ser Pro Ser Ser Thr Asn Cys
20 25 30
His Pro Tyr Thr Phe Ala Pro Pro Pro Gln Ala Gly
35 40

(2) INFORMATION FOR SEQ ID NO:18:

5

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

10

Ser Gly Phe Trp Glu Phe Ser Arg Gly Leu Trp Asp Gly Glu Asn Arg
1 5 10 15
Lys Ser Val Arg Ser Gly Cys Gly Phe Arg Gly Ser Ser Ala Gln Gly
20 25 30
Pro Cys Pro Val Thr Pro Ala Thr Ile Asp Lys His
35 40

(2) INFORMATION FOR SEQ ID NO:19:

15

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

20

Ser Glu Ser Gly Arg Cys Arg Ser Val Ser Arg Trp Met Thr Thr Trp
1 5 10 15
Gln Thr Gln Lys Gly Gly Cys Gly Ser Asn Val Ser Arg Gly Ser Pro
20 25 30
Leu Asp Pro Ser His Gln Thr Gly His Ala Thr Thr
35 40

(2) INFORMATION FOR SEQ ID NO:20:

25

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

30

Arg Glu Trp Arg Phe Ala Gly Pro Pro Leu Asp Leu Trp Ala Gly Pro
1 5 10 15
Ser Leu Pro Ser Phe Asn Ala Ser Ser His Pro Arg Ala Leu Arg Thr
20 25 30

Tyr Trp Ser Gln Arg Pro Arg
35

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

5

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Arg Met Glu Asp Ile Lys Asn Ser Gly Trp Arg Asp Ser Cys Arg Trp
1 5 10 15
Gly Asp Leu Arg Pro Gly Cys Gly Ser Arg Gln Trp Tyr Pro Ser Asn
10 20 25 30
Met Arg Ser Ser Arg Asp Tyr Pro Ala Gly Gly His
35 40

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

15

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ser His Pro Trp Tyr Arg His Trp Asn His Gly Asp Phe Ser Gly Ser
1 5 10 15
Gly Gln Ser Arg His Thr Pro Pro Glu Ser Pro His Pro Gly Arg Pro
20 25 30
20 Asn Ala Thr Ile
35

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

25

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Arg Tyr Lys His Asp Ile Gly Cys Asp Ala Gly Val Asp Lys Lys Ser
1 5 10 15
Ser Ser Val Arg Gly Gly Cys Gly Ala His Ser Ser Pro Pro Arg Ala
20 25 30
Gly Arg Gly Pro Arg Gly Thr Met Val Ser Arg Leu
35 40

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(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ser Gln Gly Ser Lys Gln Cys Met Gln Tyr Arg Thr Gly Arg Leu Thr
1 5 10 15
Val Gly Ser Glu Tyr Gly Cys Gly Met Asn Pro Ala Arg His Ala Thr
20 25 30
Pro Ala Tyr Pro Ala Arg Leu Leu Pro Arg Tyr Arg
35 40

(2) INFORMATION FOR SEQ ID NO:25:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

15 Ser Gly Arg Thr Thr Ser Glu Ile Ser Gly Leu Trp Gly Trp Gly Asp
1 5 10 15
Asp Arg Ser Gly Tyr Gly Trp Gly Asn Thr Leu Arg Pro Asn Tyr Ile
20 25 30
Pro Tyr Arg Gln Ala Thr Asn Arg His Arg Tyr Thr
35 40

(2) INFORMATION FOR SEQ ID NO:26:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

25 Arg Trp Asn Trp Thr Val Leu Pro Ala Thr Gly Gly His Tyr Trp Thr
1 5 10 15
Arg Ser Thr Asp Tyr His Ala Ile Asn Asn His Arg Pro Ser Ile Pro
20 25 30
His Gln His Pro Thr Pro Ile
35

(2) INFORMATION FOR SEQ ID NO:27:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Ser Trp Ser Ser Trp Asn Trp Ser Ser Lys Thr Thr Arg Leu Gly Asp
1 5 10 15
5 Arg Ala Thr Arg Glu Gly Cys Gly Pro Ser Gln Ser Asp Gly Cys Pro
20 25 30
Tyr Asn Gly Arg Leu Thr Thr Val Lys Pro Arg Thr
35 40

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

10

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Ser Gly Ser Leu Asn Ala Trp Gln Pro Arg Ser Trp Val Gly Gly Ala
1 5 10 15
Phe Arg Ser His Ala Asn Asn Asn Leu Asn Pro Lys Pro Thr Met Val
20 25 30
15 Thr Arg His Pro Thr
35

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

20

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Arg Tyr Ser Gly Leu Ser Pro Arg Asp Asn Gly Pro Ala Cys Ser Gln
1 5 10 15
Glu Ala Thr Leu Glu Gly Cys Gly Ala Gln Arg Leu Met Ser Thr Arg
20 25 30
25 Arg Lys Gly Arg Asn Ser Arg Pro Gly Trp Thr Leu
35 40

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

30

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Ser Val Gly Asn Asp Lys Thr Ser Arg Pro Val Ser Phe Tyr Gly Arg
1 5 10 15
Val Ser Asp Leu Trp Asn Ala Ser Leu Met Pro Lys Arg Thr Pro Ser
20 25 30
Ser Lys Arg His Asp Asp Gly
35

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(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Arg Trp Pro Ser Val Gly Tyr Lys Gly Asn Gly Ser Asp Thr Ile Asp
1 5 10 15
Val His Ser Asn Asp Ala Ser Thr Lys Arg Ser Leu Ile Tyr Asn His
20 25 30
Arg Arg Pro Leu Phe Pro
35

15

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Arg Thr Phe Glu Asn Asp Gly Leu Gly Val Gly Arg Ser Ile Gln Lys
1 5 10 15
Lys Ser Asp Arg Trp Tyr Ala Ser His Asn Ile Arg Ser His Phe Ala
20 25 30
Ser Met Ser Pro Ala Gly Lys
35

(2) INFORMATION FOR SEQ ID NO:33:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

30

Ser Tyr Cys Arg Val Lys Gly Gly Glu Gly Gly His Thr Asp Ser
1 5 10 15

Asn Leu Ala Arg Ser Gly Cys Gly Lys Val Ala Arg Thr Ser Arg Leu
20 25 30
Gln His Ile Asn Pro Arg Ala Thr Pro Pro Ser Arg
35 40

(2) INFORMATION FOR SEQ ID NO:34:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

10 Ser Trp Thr Arg Trp Gly Lys His Thr His Gly Gly Phe Val Asn Lys
1 5 10 15
Ser Pro Pro Gly Lys Asn Ala Thr Ser Pro Tyr Thr Asp Ala Gln Leu
20 25 30
Pro Ser Asp Gln Gly Pro Pro
35

(2) INFORMATION FOR SEQ ID NO:35:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

20 Ser Gln Val Asp Ser Phe Arg Asn Ser Phe Arg Trp Tyr Glu Pro Ser
1 5 10 15
Arg Ala Leu Cys His Gly Cys Gly Lys Arg Asp Thr Ser Thr Thr Arg
20 25 30
Ile His Asn Ser Pro Ser Asp Ser Tyr Pro Thr Arg
35 40

(2) INFORMATION FOR SEQ ID NO:36:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

30 Ser Phe Leu Arg Phe Gln Ser Pro Arg Phe Glu Asp Tyr Ser Arg Thr
1 5 10 15
Ile Ser Arg Leu Arg Asn Ala Thr Asn Pro Ser Asn Val Ser Asp Ala
20 25 30
His Asn Asn Arg Ala Leu Ala
35

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

5 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Arg Ser Ile Thr Asp Gly Gly Ile Asn Glu Val Asp Leu Ser Ser Val
1 5 10 15
Ser Asn Val Leu Glu Asn Ala Asn Ser His Arg Ala Tyr Arg Lys His
20 25 30
Arg Pro Thr Leu Lys Arg Pro
35

10 (2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Ser Ser Lys Val Ser Ser Pro Arg Asp Pro Thr Val Pro Arg Lys Gly
1 5 10 15
Gly Asn Val Asp Tyr Gly Cys Gly His Arg Ser Ser Ala Arg Met Pro
20 25 30
Thr Ser Ala Leu Ser Ser Ile Thr Lys Cys Tyr Thr
35 40

20 (2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Arg Ala Ser Thr Gln Gly Gly Arg Gly Val Ala Pro Glu Phe Gly Ala
1 5 10 15
Ser Val Leu Gly Arg Gly Cys Gly Ser Ala Thr Tyr Tyr Thr Asn Ser
20 25 30
Thr Ser Cys Lys Asp Ala Met Gly His Asn Tyr Ser
35 40

(2) INFORMATION FOR SEQ ID NO:40:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

5 Arg Trp Cys Glu Lys His Lys Phe Thr Ala Ala Arg Cys Ser Ala Gly
1 5 10 15
Ala Gly Phe Glu Arg Asp Ala Ser Arg Pro Pro Gln Pro Ala His Arg
20 25 30
Asp Asn Thr Asn Arg Asn Ala
35

(2) INFORMATION FOR SEQ ID NO:41:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

15 Ser Phe Gln Val Tyr Pro Asp His Gly Leu Glu Arg His Ala Leu Asp
1 5 10 15
Gly Thr Gly Pro Leu Tyr Ala Met Pro Gly Arg Trp Ile Arg Ala Arg
20 25 30
Pro Gln Asn Arg Asp Arg Gln
35

(2) INFORMATION FOR SEQ ID NO:42:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

25 Ser Arg Cys Thr Asp Asn Glu Gln Cys Pro Asp Thr Gly Thr Arg Ser
1 5 10 15
Arg Ser Val Ser Asn Ala Arg Tyr Phe Ser Ser Arg Leu Leu Lys Thr
20 25 30
His Ala Pro His Arg Pro
35

(2) INFORMATION FOR SEQ ID NO:43:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Ser Ala Arg Asp Ser Gly Pro Ala Glu Asp Gly Ser Arg Ala Val Arg
1 5 10 15
Leu Asn Gly Val Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg Ser Asn
20 25 30
5 Pro Arg Gly Arg Arg His Pro
35

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

10

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Ser Ser Ala Asp Ala Glu Lys Cys Ala Gly Ser Leu Leu Trp Trp Gly
1 5 10 15
Arg Gln Asn Asn Ser Gly Cys Gly Ser Pro Thr Lys Lys His Leu Lys
20 25 30
His Arg Asn Arg Ser Gln Thr Ser Ser Ser Ser His
35 40

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(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

20

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Arg Pro Lys Asn Val Ala Asp Ala Tyr Ser Ser Gln Asp Gly Ala Ala
1 5 10 15
Ala Glu Glu Thr Ser His Ala Ser Asn Ala Ala Arg Lys Ser Pro Lys
20 25 30
His Lys Pro Leu Arg Arg Pro
35

25

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Arg Gly Ser Thr Gly Thr Ala Gly Gly Glu Arg Ser Gly Val Leu Asn
1 5 10 15
Leu His Thr Arg Asp Asn Ala Ser Gly Ser Gly Phe Lys Pro Trp Tyr
20 25 30
Pro Ser Asn Arg Gly His Lys
35

(2) INFORMATION FOR SEQ ID NO:47:

5

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

10

Arg Trp Gly Trp Glu Arg Ser Pro Ser Asp Tyr Asp Ser Asp Met Asp
1 5 10 15
Leu Gly Ala Arg Arg Tyr Ala Thr Arg Thr His Arg Ala Pro Pro Arg
20 25 30
Val Leu Lys Ala Pro Leu Pro
35

(2) INFORMATION FOR SEQ ID NO:48:

15

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

20

Arg Gly Trp Lys Cys Glu Gly Ser Gln Ala Ala Tyr Gly Asp Lys Asp
1 5 10 15
Ile Gly Arg Ser Arg Gly Cys Gly Ser Ile Thr Lys Asn Asn Thr Asn
20 25 30
His Ala His Pro Ser His Gly Ala Val Ala Lys Ile
35 40

(2) INFORMATION FOR SEQ ID NO:49:

25

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

30

Ser Arg Glu Glu Ala Asn Trp Asp Gly Tyr Lys Arg Glu Met Ser His
1 5 10 15
Arg Ser Arg Phe Trp Asp Ala Thr His Leu Ser Arg Pro Arg Arg Pro
20 25 30

Ala Asn Ser Gly Asp Pro Asn
35

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

5

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Glu Trp Tyr Ser Trp Lys Arg Ser Ser Lys Ser Thr Gly Leu Gly Asp
1 5 10 15
Thr Ala Thr Arg Glu Gly Cys Gly Pro Ser Gln Ser Asp Gly Cys Pro
10 20 25 30
Tyr Asn Gly Arg Leu Thr Thr Val Lys Pro Arg Lys
35 40

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

15

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Arg Glu Phe Ala Glu Arg Arg Leu Trp Gly Cys Asp Asp Leu Ser Trp
1 5 10 15
Arg Leu Asp Ala Glu Gly Cys Gly Pro Thr Pro Ser Asn Arg Ala Val
20 25 30
20 Lys His Arg Lys Pro Arg Pro Arg Ser Pro Ala Leu
35 40

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

25

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys Glu
1 5 10 15
Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly Arg Lys
20 25 30
30 Val Phe Asn Arg Arg Pro Ser Ala Ile Pro Thr
35 40

30

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Arg His Ile Ser Glu Tyr Ser Phe Ala Asn Ser His Leu Met Gly Gly
1 5 10 15
Glu Ser Lys Arg Lys Gly Cys Gly Ile Asn Gly Ser Phe Ser Pro Thr
20 25 30
Cys Pro Arg Ser Pro Thr Pro Ala Phe Arg Arg Thr
35 40

(2) INFORMATION FOR SEQ ID NO:54:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Ser Arg Glu Ser Gly Met Trp Gly Ser Trp Trp Arg Gly His Arg Leu
1 5 10 15
Asn Ser Thr Gly Gly Asn Ala Asn Met Asn Ala Ser Leu Pro Pro Asp
20 25 30
Pro Pro Val Ser Thr Pro
35

(2) INFORMATION FOR SEQ ID NO:55:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp
1 5 10 15
Ser Asp Ser Asp Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu
20 25 30
Arg Thr Arg Ser Arg Pro Asn
35

(2) INFORMATION FOR SEQ ID NO:56:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:
 TCTCACTCCT CGAGATCCGG CGCTTATGAG AGTCCGGATG GTCGGGGGGG TCGGAGCTAT 60
 GTGGGGGGCG GGGGTGGNTG TGGTAACATT GGTCGGAAGC ATAACCTGTG GGGGCTGCGT 120
 5 ACCCGTGCAGC CGGCCTGCTG GGACTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA 177

(2) INFORMATION FOR SEQ ID NO:57:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:
 TCTCACTCCT CGAGTCCTCG CTCTTTCTGG CCCGTTGTGT CCCGGCATGA GTCGTTGGG 60
 ATCTCTAACT ATTTGGGNTG TGGTATCGT ACATGTATCT CCGGCACGAT GACTAAGTCT 120
 AGCCCCGATT ACCCTCGGCA TTCGTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA 177

(2) INFORMATION FOR SEQ ID NO:58:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:
 TCTCACTCCT CGAGTAGTAG CTCCGATTGG GGTGGTGTGC CTGGGAAGGT GGTTAGGGAG 60
 20 CGCTTAAAGG GGCGCGGTTG TGGTATTTCG ATCACCTCCG TGCTCACTGG GAAGCCAAT 120
 CCGTGTCCGG AGCCTAAGGC GCCCTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA 177

(2) INFORMATION FOR SEQ ID NO:59:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:
 TCTCACTCCT CGAGAGTTGG CCAGTGCACG GATTCTGATG TGCAGCGTCC TTGGGCCAGG 60
 TCTTGCGCTC ATCAGGGTTG TGGTGCAGGC ACTCGCAACT CGCACGGCTG CATCACCCGT 120
 CCTCTCCGCC AGGCTAGCGC TCATTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA 177

(2) INFORMATION FOR SEQ ID NO:60:
 30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

5 TCTCACTCCT CGAGCCACTC CGGTGGTATG AATAGGGCCT ACGGGGATGT GTTTAGGGAG 60
 CTCGTGATC GGTGGAACGC CACTTCCCAC CACACTCGCC CCACCCCTCA GCTCCCCCGT 120
 GGCCTAATT CTAGAACATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 168 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

TCTCACTCCT CGAGTCCGTG CGGGGGGTG TGCGGGCGTT TTATGCAGGG TGGCCTTTTC 60
 GCGGTAGGA CTGATGGTTG TGGTGCCCAT AGAAACCGCA CTTCTGCGTC GTTAGAGCCC 120
 CCGAGCAGCG ACTACTCTAG AATCGAAGGT CGCGCTAGAC CTTCGAGA 168

15 (2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

TCTCACTCCT CGAGGGCGC CGCCGATCAG CGGCGGGGGT GGTCCGAGAA CTTGGGGTTG 60
 CCTAGGGTGG GGTGGGACGC CATCGCTCAC AATAGCTATA CGTTCACCTC GCGCCGCCCG 120
 CGCCCCCCT CTAGA 135

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

25 TCTCACTCCT CGAGCGGTGG GGAGGTCAGC TCCTGGGGCC GCGTGAATGA CCTCTGCGCT 60
 AGGGTGAGTT GGACTGGTTG TGGTACTGCT CGTTCCGCGC GTACCGACAA CAAAGGCTTT 120
 CTTCCTAAGC ACTCGTCACT CCGCTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA 177

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

TCTCACTCCT CGAGTGATAG TGACGGGGAT CATTATGGGC TTTCGGGGGG GGTGCGTTGT	60
TCGCTTCGTG ATAGGGGTTG TGGTCTGGCC CTGTCCACCG TCCATGCTGG TCCCCCCTCT	120
TTTACCCCCA AGCTCTCCAG CCCCTCTAGA ATCGAAGGTC GCGCTAGACC TTCCGAGA	177

(2) INFORMATION FOR SEQ ID NO:65:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TCTCACTCCT CGAGGAGCTT GGGTAATTAT GGCGTCACCG GGAAGTGTGGA CGTGACGGTT	60
TTGCCCATGTC CTGGCCACGC CAACCACCTT GGTGCTCTCT CCGCCTCTAG CTCTGATCCT	120
CCGCAGCGCT CTAGAACATCGA AGGTCGCGCT AGACCTTCGA GA	162

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

TCTCACTCCT CGAGAACTAC GACGGCTAAC GGGTGTCTTC TCGGAAGCTT CGGCAGTTCTT	60
AGTGGGTGCT CATTACGCC AACCTCTCCA CCGCCCCACC TAGGATAACCC CCCCCACTCC	120
GTCAATTCTA GAATCGAAGG TCGCGCTAGA CCTTCGAGA	159

25 (2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

TCTCACTCCT CGAGCCCCGAA GTTGTCCAGC GTGGGTGTTA TGACTAAGGT CACGGAGCTG	60
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CCCACGGAGG GGCCTAACGC CATTAGTATT CCGATCTCCG CGACCCTCGG CCCGCGCAAC 120
CCGCTCCGCT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

TCTCACTCCT CGAGGTGGTG CGGCGCTGAG CTGTGCAACT CGGTGACTAA GAAGTTTCGC 60
CCGGGCTGGC GGGATCACGC CAATCCCTCC ACCCATCATC GTACTCCCCC GCCCAGGCCAG
TCCAGCCCTT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 120
162

10 (2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

TCTCACTCCT CGAGGTGGTG CGGCGCTGAT GACCCGTGTG GTGCCAGTCG TTGGCGGGGG 60
GGCAACAGCT TGTTTGGTTG TGGTCTTCGT TGTAGTGCAG CGCAGAGCAC CCCGAGTGGC
AGGATCCATT CCACTTCGAC CAGCTCTAGA ATCGAAGGTG CGCTAGACCT TCGAGA 120
176

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

TCTCACTCCT CGAGTAAGTC CGGGGAGGGG GGTGACAGTA GCAGGGGCGA GACGGGCTGG 60
GCGAGGGTTC GGTCTCACGC CATGACTGCT GGCCGTTTC GGTGGTACAA CCAGTTGCC
25 TCTGATCGGT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 120
162

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

TCTCACTCCT	CGAGGTCGAG	CGCCAATAAT	TGCGAGTGG	AGTCTGATTG	GATGCGCAGG	60
GCCTGTATTG	CTCGTTACGC	CAACAGTCG	GGCCCCGCC	GCGCCGTCGA	CACTAAGGCC	120
CGCCCTCTA	GAATCGAAGG	TCGCGCTAGA	CCTTCGAGA			159

(2) INFORMATION FOR SEQ ID NO:72:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

10 TCTCACTCCT	CGAGTAAGTG	GTCGTGGAGT	TCGAGGTGG	GCTCCCCGCA	GGATAAGGTT	60
GAGAAGACCA	GGGCGGGTTG	TGGTGGTAGT	CCCAGCAGCA	CCAATTGTCA	CCCCTACACC	120
TTTGCCCCCC	CCCCGCAAGC	CGGCTCTAGA	ATCGAAGGTC	GCGCTAGACC	TTCGAGA	177

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

TCTCACTCCT	CGAGTGGTT	CTGGGAGTT	AGCAGGGGC	TTTGGGATGG	GGAGAACCGT	60
AAGAGTGTCC	GGTCGGGTTG	TGGTTTTCGT	GGCTCTCTG	CTCAGGGCCC	GTGTCGGTC	120
ACGCCTGCCA	CCATTGACAA	ACACTCTAGA	ATCGAAGGTC	GCGCTAGACC	TTCGAGA	177

20 (2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

TCTCACTCCT	CGAGTGAGAG	CGGGCGGTGC	CGTAGCGTGA	GCCGGTGGAT	GACGACGTGG	60
CAGACGCAGA	AGGGCGGTTG	TGGTCCAAT	GTTTCCCGCG	GTTCGCCCT	CGACCCCTCT	120
CACCAGACCG	GGCATGCCAC	TACTTCTAGA	ATCGAAGGTC	GCGCTAGACC	TTCGAGA	177

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

TCTCACTCCT CGAGGGAGTG GAGGTTGCC GGGCCGCCGT TGGACCTGTG GGCGGGTCCG AGCTTGCCT CTTTAACGC CAGTTCCAC CCTCGCGCCC TGCGCACCTA TTGGTCCCAG CGGCCCCGCT CTAGAACATCGA AGGTCGCGCT AGACCTTCGA GA	60 120 162
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5 (2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

TCTCACTCCT CGAGGATGGA GGACATCAAG AACTCGGGGT GGAGGGACTC TTGTAGGTGG GGTAGCTGA GGCCTGGTTG TGGTAGCCGC CAGTGGTACC CCTCGAATAT GCGTTCTAGC AGAGATTACC CCGCGGGGGG CCACTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA	60 120 177
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(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

TCTCACTCCT CGAGTCATCC GTGGTACAGG CATTGGAACC ATGGTGACTT CTCTGGTTCG GGCAGTCAC GCCACACCCC GCCGGAGAGC CCCCACCCCCG CCCGCCCTAA TGCCACCATT TCTAGAACATCG AAGGTCGCGC TAGACCTTCG AG	60 120 152
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20 (2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

TCTCACTCCT CGAGATATAA GCACGATATC GGTTGCGATG CTGGGGTTGA CAAGAACGTCG TCGTCTGTGC GTGGTGTTG TGTTGCTCAT TNGTCGCCAC CCCGCGCCGG CCCTGGTCCT CGCGGCACGA TGGTTAGCAG GCTTTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA	60 120 177
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(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

5 TCTCACTCCT CGAGTCAGGG CTCCAAGCAG TGTATGCAGT ACCGCACCGG TCGTTTGACG 60
 GTGGGGTCTG AGTATGGTTG TGGTATGAAC CCCGCCGCC ATGCCACGCC CGCTTATCCG 120
 GCGCGCCTGC TGCCACGCTA TCGCTCTAGA ATCGAAGGTC GCGCTAGACC TTGAGA 177

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TCTCACTCCT CGAGTGGCG GACTACTAGT GAGATTTCTG GGCTCTGGGG TTGGGGTGAC 60
 GACCGGAGCG GTTATGGTTG GGGTAACACG CTCCGCCCA ACTACATCCC TTATAGGCAG 120
 GCGACGAACA GGCATCGTTA TACGTCTAGA ATCGAAGGTC GCGCTAGACC TTGAGA 177

(2) INFORMATION FOR SEQ ID NO:81:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 162 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

20 TCTCACTCCT CGAGGTGGAA TTGGACTGTC TTGCCGCCA CTGGCGGCCA TTACTGGACG 60
 CGTCGACGG ACTATCACGC CATTAACAAT CACAGGCCGA GCATCCCCA CCAGCATCCG 120
 ACCCTATCT CTAGAACCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

TCTCACTCCT CGAGTTGGTC GTCTGGAAAT TGGAGCTCTA AGACTACTCG TCTGGGGGAC 60
 AGGGCGACTC GGGAGGGTTG TGGTCCCAGC CAGTCTGATG GCTGTCCTTA TAACGGCCGC 120
 CTTACGACCG TCAAGCCTCG CACGTCTAGA ATCGAAGGTC GCGCTAGACC TTGAGA 177

30 (2) INFORMATION FOR SEQ ID NO:83:

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 156 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA	
5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:	
	TCTCACTCCT CGAGTGGTAG TTTGAACGCA TGGCAACCGC GGTCATGGGT GGGGGCGCG TTCCGGTCAC ACGCCAACAA TAACTTGAAC CCCAAGCCA CCATGGTTAC TNNTCACCT ACCTCTAGAA TCGAAGGTCG CGCTAGACCT TCGAGA	60 120 156
	(2) INFORMATION FOR SEQ ID NO:84:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 178 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:	
	TCTCACTCCT CGAGGTATTG GGGTTTGTC CCGCGGGACA ACGGTCCCAG TTGTAGTCAG GAGGCTACCT TGGAGGGTTG TGGTGCGCAG AGGCTGATGT CCACCCGTCG CAAGGGCGC AACTCCCGCC CCGGGTGGAC GCTCTCTAGA ATCGAAGGTC GCGCTAGACC CTTCGAGA	60 120 178
15	(2) INFORMATION FOR SEQ ID NO:85:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 162 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:	
	TCTCACTCCT CGAGCGTGGG GAATGATAAG ACTAGCAGGC CGGTTTCCTT CTACGGCGC GTTAGTGATC TGTGGAACGC CAGCTTGATG CCGAAGCGTA CTCCAGCTC GAAGGCCAC GATGATGGCT CTAGAACATCGA AGGTCGCGCT AGACCTTCGA GA	60 120 162
	(2) INFORMATION FOR SEQ ID NO:86:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 162 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:	
30	TCTCACTCCT CGAGTACTCC CCCCAGTAGG GAGGCGTATA GTAGGCCCTA TAGTGTGAT AGCGATTGG ATACGAACGC CAAGCACAGC TCCCACAAACC GCCGTNTGCG GACGCGCAGC CGCCCGAACT CTAGAACATCGA AGGTCGCGCT AGACCTTCGA GA	60 120 162

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

TCTCACTCCT CGAGATGGCC TAGTGTGGGT TACAAGGGTA ATGGCAGTGA CACTATTGAT 60
GTTCACAGCA ATGACGCCAG TACTAAGAGG TCCCTCATCT ATAACCACCG CCGCCCCNTC 120
TTTCCCTCTA GAATCGAAGG TCGCGCTAGA CCTTCGAGA 159

(2) INFORMATION FOR SEQ ID NO:88:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

15 TCTCACTCCT CGAGAACGTT TGAGAACGAC GGGCTGGGCG TCGGCCGGTC TATTCAAAG 60
AAGTCGGATA GGTGGTACGC CAGCCACAAAC ATTCTAGGC ATTCGCGTC CATGTCTCCC 120
GCTGGTAAGT CTAGAACATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

TCTCACTCCT CGAGCTATTG TCGGGTTAAC GGTGGTGGGG AGGGGGGGCA TACGGATTCC 60
AATCTGGCTA GGTCGGGTTG TGGAAGGTG GCCAGGACCA GCAGGCTTCA GCATATCAAC 120
CCGCGCGCTA CCCCCCCCCC CCGGTCTAGA ATCGAAGGTC 160

25 (2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

30 TCTCACTCCT CGAGTTGGAC TCGGTGGGGC AAGCACANTC ATGGGGGGTT TGTGAACAAG 60

TCTCCCCCTG GGAAGAACGC CACGAGCCCC TACACCGACG CCCAGCTGCC CAGTGATCAG 120
GGTCCTCCCT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TCTCACTCCT CGAGTCAGGT TGATTCGTT CGTAATAGCT TTCGGTGGTA TGAGCCGAGC 60
AGGGCTCTGT GCCATGGTTG TGGTAAGCGC GACACCTCCA CCACTCGTAT CCACAATAGC
CCCAGCGACT CCTATCCTAC ACGCTCTAGA ATCGAAGGTC GCGCTAGACC TTGAGA 120
177

10 (2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

TCTCACTCCT CGAGCTTTT GCGGTTCCAG AGTCCGAGGT TCGAGGATTA CAGTAGGACG 60
ATCTNTCGGT TGCGAACGC CACGAACCCG AGTAATGTCT CCGATGCGCA CAATAACCGG
GCCTTGGCCT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 120
162

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

TCTCACTCCT CGAGGAGCAT CACCGACGGG GGCATCAATG AGGTGGACCT GAGTAGTGTG 60
TCGAACGTTT TTGAGAACGC CAACTCGCAT AGGGCCTACA GGAAGCATCG CCCGACCTTG
AAGCGTCCTT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 120
162

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

TCTCACTCCT CGAGTTCGAA GGTGAGCAGC CCGAGGGATC CGACGGTCCC GCGBAAGGGC	60
GGCAATGTTG ATTATGTTG TGGTCACAGG TCTTCGCCCG GGATGCCTAC CTCCGCTCTG	120
TCGTCGATCA CGAAGTGCTA CACTTCTAGA ATCGAAGGTC GCGCTAGACC TTGAGA	177

(2) INFORMATION FOR SEQ ID NO:95:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TCTCACTCCT CGAGAGCCAG TANGCAGGGC GGCCGGGGTG TTGCCCTGA GTTGGGGCG	60
AGCGTTTTGG GTNGTGGTTG TGTTAGCGCC ACTTATTACA CGAACTCCAC CAGCTGCAAG	120
GATGCTATGG GCCACAACTA CTCGTCTAGA ATCGAAGGTC GCGNTAGACC TTGAGA	177

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

TCTCACTCCT CGAGATGGTG CGAGAACAC AAGTTACGG CTGCGCGTTG CAGCGCGGGG	60
GCGGGTTTG AGAGGGANGC CAGCCGTCCG CCCCAGCCTG CCCACCGGGA TAATACCAAC	120
CGTAATGCNT NTAGAATCGA AGGTCGCGCT AGACCTTCGA GA	162

20 (2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

TCTCACTCCT CGAGTTTCA GGTGTACCCG GACCATGGTC TGGAGAGGCA TGCTTTGGAC	60
GGGACGGGTC CGCTTTACGC CATGCCCGC CGCTGGATTA GGGCGCGTCC GCAGAACAGG	120
GACCGCCAGT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA	162

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

TCTCACTCCT CGAGCAGGTG TACGGACAAC GAGCAGTGCC CCGATACCGG GANTAGGTCT 60
CGTCCGTTA GTAACGCCAG GTACTTTCG AGCAGGTTGC TCAAGACTCA CGCCCCCAT 120
CGCCCTTCTA GAATCGAAGG TCGCGCTAGA CCTTCGAGA 159

5 (2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

TCTCACTCCT CGAGTGCAG GGATAGCGGG CCTGCGGAGG ATGGGTCCCG CGCCGTCCGG 60
TTGAACGGGG TTGAGAACGC CAACACTAGG AAGTCCTCCC GCAGTAACCC GCGGGGTAGG 120
CGCCATCCCT CTAGAACATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

TCTCACTCCT CGAGTTCCGC CGATGCGGAG AAGTGTGCGG GCAGTCTGTT GTGGTGGGGT 60
AGGCAGAACCA ACTCCGGTTG TGTTCGCCC ACGAAGAACG ATCTGAAGCA CCGCAATCGC 120
AGTCAGACCT CCTCTTCGTC CCACCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA 177
20

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TCTCACTCCT CGAGACCGAA GAACGTGGCC GATGCTTATT CGTCTCAGGA CGGGCGGGCG 60
GCCGAGGAGA CGTCTCACGC CAGTAATGCC GCGCGGAAGT CCCCTAACGCA CAAGCCCTTG 120
AGGCAGGCCTT CTAGAACATCGA AGGTCGCGCT AGACCTTCGA GA 162
30

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

5 TCTCACTCCT CGAGAGGCAG TACGGGGACG GCCGGCGCG AGCGTTCCGG GGTGCTCAAC 60
 CTGACACCCA GGGATAACGC CAGCGGCAGC GGTTCAAAC CGTGGTACCC TTCAATCGG 120
 GGTACACAAGT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 162 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

TCTCACTCCT CGAGGTGGGG GTGGGAGAGG AGTCCGTCG ACTACGATTG TGATATGGAC 60
 TTGGGGCGA GGAGGTACGC CACCCGCACC CACCGCGCG CCCCTCGCGT CTTGAAGGCT 120
 CCCCTGCCCT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO:104:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

20 TCTCACTCCT CGAGGCACTG GAAAGTGCAGG GGCTCTCAGG CTGCCTACGG GGACAAGGAT 60
 ATCGGGAGGT CCAGGGGTTG TGTTCCATT ACAAAAGAATA ACACAAATCA CGCCCATCCT 120
 AGCCACGGCG CGTGTCTAA GATCTCTAGA ATCGAAGGTC GCGCTAGACC TTGAGA 177

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 162 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

TCTCACTCCT CGAGCCGCGA GGAGGCGAAC TGGGACGGCT ATAAGAGGGA GATGAGCCAC 60
 CGGAGTCGCT TTTGGGACGC CACCCACCTG TCCCACCTC GCCGCCCCGC TAACTCTGGT 120
 GACCCTAACT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

30 (2) INFORMATION FOR SEQ ID NO:106:

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 177 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA	
5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:	
	TCTCACTCNT CGAGAGAGTT CGCGGAGAGG AGGTTGTGGG GGTGTGATGA CCTGAGTTGG CGTCTCGACG CGGAGGGTTG TGGTCCCACT CCGAGCAATC GGGCCGTCAA GCATCGCAAG CCCCGCCAAC GCTCCCCCGC ACTCTCTAGA ATCGAAGGTC GCGCTAGACC TTGAGA	60 120 177
	(2) INFORMATION FOR SEQ ID NO:107:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 177 base pairs	
10	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:	
	TCTCACTCNT NGAGTGATCA CGCGTTGGGG ACGAATCTGA GGTCTGACAA TGCCAAGGAG CCGGGTGATT ACAACTGTTG TGGTAACGGG AACTCTACCG GGCAGAAAGGT TTTAACCGT 15 AGGCGCCCT CCGCCATCCC CANTTCTAGA ATCGAAGGTC GCGCTAGACC TTGAGA	60 120 177
	(2) INFORMATION FOR SEQ ID NO:108:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 177 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:	
	TCTCACTCCT CGAGGCATAT TTCTGAGTAT AGCTTGCGA ATTCCCACTT GATGGGTGGC GAGTCCAAGC GGAAGGGTTG TGGTATTAAC GGCTCCTTT CTCCCACTTG TCCCCGCTCC CCCACCCAG CCTTCCGCCG CACCTCTAGA ATCGAAGGTC GCGCTAGACC TTGAGA	60 120 177
	(2) INFORMATION FOR SEQ ID NO:109:	
	(i) SEQUENCE CHARACTERISTICS:	
25	(A) LENGTH: 158 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:	
30	TCTCACTCCT CGAGCCGGGA GAGCGGGATG TGGGGTAGTT GGTGGCGTGG TCACAGGTTG AATTCCACGG GGGGTAACGC CAACATGAAT GCTAGTCTGC CCCCCGACCC CCCTGTTCC ACTCCGTCTA GAATCGAAGG TCGCGCTAGA CCTTCGAG	60 120 158

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 708 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

5 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Met Gly Met Ser Lys Ser His Ser Phe Phe Gly Tyr Pro Leu Ser Ile
1 5 10 15
Phe Phe Ile Val Val Asn Glu Phe Cys Glu Arg Phe Ser Tyr Tyr Gly
20 25 30
Met Arg Ala Ile Leu Ile Leu Tyr Phe Thr Asn Phe Ile Ser Trp Asp
35 40 45
10 Asp Asn Leu Ser Thr Ala Ile Tyr His Thr Phe Val Ala Leu Cys Tyr
50 55 60
Leu Thr Pro Ile Leu Gly Ala Leu Ile Ala Asp Ser Trp Leu Gly Lys
65 70 75 80
Phe Lys Thr Ile Val Ser Leu Ser Ile Val Tyr Thr Ile Gly Gln Ala
85 90 95
Val Thr Ser Val Ser Ser Ile Asn Asp Leu Thr Asp His Asn His Asp
100 105 110
Gly Thr Pro Asp Ser Leu Pro Val His Val Val Leu Ser Leu Ile Gly
115 120 125
15 Leu Ala Leu Ile Ala Leu Gly Thr Gly Gly Ile Lys Pro Cys Val Ser
130 135 140
Ala Phe Gly Gly Asp Gln Phe Glu Glu Gly Gln Glu Lys Gln Arg Asn
145 150 155 160
Arg Phe Phe Ser Ile Phe Tyr Leu Ala Ile Asn Ala Gly Ser Leu Leu
165 170 175
Ser Thr Ile Ile Thr Pro Met Leu Arg Val Gln Gln Cys Gly Ile His
180 185 190
Ser Lys Gln Ala Cys Tyr Pro Leu Ala Phe Gly Val Pro Ala Ala Leu
195 200 205
20 Met Ala Val Ala Leu Ile Val Phe Val Leu Gly Ser Gly Met Tyr Lys
210 215 220
Lys Phe Lys Pro Gln Gly Asn Ile Met Gly Lys Val Ala Lys Cys Ile
225 230 235 240
Gly Phe Ala Ile Lys Asn Arg Phe Arg His Arg Ser Lys Ala Phe Pro
245 250 255
Lys Arg Glu His Trp Leu Asp Trp Ala Lys Glu Lys Tyr Asp Glu Arg
260 265 270
Leu Ile Ser Gln Ile Lys Met Val Thr Arg Val Met Phe Leu Tyr Ile
275 280 285
25 Pro Leu Pro Met Phe Trp Ala Leu Phe Asp Gln Gln Gly Ser Arg Trp
290 295 300
Thr Leu Gln Ala Thr Thr Met Ser Gly Lys Ile Gly Ala Leu Glu Ile
305 310 315 320
Gln Pro Asp Gln Met Gln Thr Val Asn Ala Ile Leu Ile Val Ile Met
325 330 335
Val Pro Ile Phe Asp Ala Val Leu Tyr Pro Leu Ile Ala Lys Cys Gly
340 345 350
Phe Asn Phe Thr Ser Leu Lys Lys Met Ala Val Gly Met Val Leu Ala
355 360 365
30 Ser Met Ala Phe Val Val Ala Ala Ile Val Gln Val Glu Ile Asp Lys
370 375 380
Thr Leu Pro Val Phe Pro Lys Gly Asn Glu Val Gln Ile Lys Val Leu

	385	390	395	400
	Asn Ile Gly Asn Asn Thr Met Asn Ile Ser Leu Pro Gly Glu Met Val			
	405	410	415	
	Thr Leu Gly Pro Met Ser Gln Thr Asn Ala Phe Met Thr Phe Asp Val			
	420	425	430	
	Asn Lys Leu Thr Arg Ile Asn Ile Ser Ser Pro Gly Ser Pro Val Thr			
	435	440	445	
5	Ala Val Thr Asp Asp Phe Lys Gln Gly Gln Arg His Thr Leu Leu Val			
	450	455	460	
	Trp Ala Pro Asn His Tyr Gln Val Val Lys Asp Gly Leu Asn Gln Lys			
	465	470	475	480
	Pro Glu Lys Gly Glu Asn Gly Ile Arg Phe Val Asn Thr Phe Asn Glu			
	485	490	495	
	Leu Ile Thr Ile Thr Met Ser Gly Lys Val Tyr Ala Asn Ile Ser Ser			
	500	505	510	
	Tyr Asn Ala Ser Thr Tyr Gln Phe Phe Pro Ser Gly Ile Lys Gly Phe			
	515	520	525	
10	Thr Ile Ser Ser Thr Glu Ile Pro Pro Gln Cys Gln Pro Asn Phe Asn			
	530	535	540	
	Thr Phe Tyr Leu Glu Phe Gly Ser Ala Tyr Thr Tyr Ile Val Gln Arg			
	545	550	555	560
	Lys Asn Asp Ser Cys Pro Glu Val Lys Val Phe Glu Asp Ile Ser Ala			
	565	570	575	
	Asn Thr Val Asn Met Ala Leu Gln Ile Pro Gln Tyr Phe Leu Leu Thr			
	580	585	590	
	Cys Gly Glu Val Val Phe Ser Val Thr Gly Leu Glu Phe Ser Tyr Ser			
	595	600	605	
15	Gln Ala Pro Ser Asn Met Lys Ser Val Leu Gln Ala Gly Trp Leu Leu			
	610	615	620	
	Thr Val Ala Val Gly Asn Ile Ile Val Leu Ile Val Ala Gly Ala Gly			
	625	630	635	640
	Gln Phe Ser Lys Gln Trp Ala Glu Tyr Ile Leu Phe Ala Ala Leu Leu			
	645	650	655	
	Leu Val Val Cys Val Val Phe Ala Ile Met Ala Arg Phe Tyr Thr Tyr			
	660	665	670	
	Ile Asn Pro Ala Glu Ile Glu Ala Gln Phe Asp Glu Asp Glu Lys Lys			
	675	680	685	
20	Asn Arg Leu Glu Lys Ser Asn Pro Tyr Phe Met Ser Gly Ala Asn Ser			
	690	695	700	
	Gln Lys Gln Met			
	705			

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

25 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

TCCGGACTCT CATAAGCGCC GG

22

(2) INFORMATION FOR SEQ ID NO:112:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:
- ACAAACGGGCC AGAAAAGAGCG AG 22
- 5 (2) INFORMATION FOR SEQ ID NO:113:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:
- ACACCCACCCCC AATCGGAGCT AC 22
- (2) INFORMATION FOR SEQ ID NO:114:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:
- TCAGAATCCG TGCACGGGCC AA 22
- (2) INFORMATION FOR SEQ ID NO:115:
- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:
- 25 GCCCTATTCA TACCACCGGA GT 22
- (2) INFORMATION FOR SEQ ID NO:116:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:
CATCAGTCCT ACCGCCGAAA AG 22

(2) INFORMATION FOR SEQ ID NO:117:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:
CGTATAGCTA TTGTGAGCGA TG 22

10 (2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:
ACGCGCGGAA CGAGCAGTAC CA 22

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:
CCATAATGAT CCCCCGTCACT AT 22

(2) INFORMATION FOR SEQ ID NO:120:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:
AGACACCCCT TAGCCGTCGT AG 22

30 (2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:
AGCTCCGTGA CCTTAGTCAT AA 22
- (2) INFORMATION FOR SEQ ID NO:122:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
10 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:
TGCACAGCTC AGCGCCGCAC CA 22
- (2) INFORMATION FOR SEQ ID NO:123:
- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:
20 ACGGGTCATC AGCGCCGCAC CA 22
- (2) INFORMATION FOR SEQ ID NO:124:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 25 (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:
TGTCACCCCC CTCCCCGGAC TT 22
- (2) INFORMATION FOR SEQ ID NO:125:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:
ACTCGCAATT ATTGGCGCTC GA 22

(2) INFORMATION FOR SEQ ID NO:126:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:
10 GTCTTCTCAA CCTTATCCTG CG 22

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:
AAAGCCCCCT GCTAAACTCC CA 22

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
20 (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:
CTGCGTCTGC CACGTCGTCA TC 22

(2) INFORMATION FOR SEQ ID NO:129:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:
30 GTTAAAAGAG GGCAAGCTCG GA 22

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

CCGAGTTCTT GATGTCCTCC AT

22

(2) INFORMATION FOR SEQ ID NO:131:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

TCCAATGCCT GTACCACCGA TG

22

15 (2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

TCGCAACCGA TATCGTGCTT AT

22

(2) INFORMATION FOR SEQ ID NO:133:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

TGCATACACT GCTTGGAGCC CT

22

(2) INFORMATION FOR SEQ ID NO:134:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GAAATCTCAC TAGTAGTCG C C 22

5 (2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

GCGGGCAAGA CAGTCCAATT C C 22

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GAGCTCCAAT TCCACGACGA C C 22

(2) INFORMATION FOR SEQ ID NO:137:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

25 GGTTGCCATG CGTTCAAAC T AC 22

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:
TCCCGCGGGG ACAAACCGA AT 22

(2) INFORMATION FOR SEQ ID NO:139:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:
CTGCTAGTCT TATCATTCCC CA 22

10 (2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:
CTATCGACAC TATAAGGCCT AC 22

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:
TACCCTTGTA ACCCACACTA GG 22

(2) INFORMATION FOR SEQ ID NO:142:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:
TTCTTCTGAA TAGACCGGCC GA 22

30 (2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:
- CCACCACCCCT TAACCCGACA AT 22
- (2) INFORMATION FOR SEQ ID NO:144:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
10 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:
- AGGGGGAGAC TTGTTCACAA AC 22
- (2) INFORMATION FOR SEQ ID NO:145:
- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:
- 20 CGGCTCATAC CACCGAAAGC TA 22
- (2) INFORMATION FOR SEQ ID NO:146:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
25 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:
- ATCGTCCTAC TGTAATCCTC GA 22
- (2) INFORMATION FOR SEQ ID NO:147:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
30 (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:
GACACACTAC TCAGGTCCAC CT 22

(2) INFORMATION FOR SEQ ID NO:148:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:
CCATAATCAA CATTGCCGCC CT 22

10 (2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:
CAAAACGCTC GCCCCAAACT CA 22

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:
GTAAACTTGT GCTTCTCGCA CC 22

(2) INFORMATION FOR SEQ ID NO:151:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:
30 CCATGGTCCG GGTACACCTG AA 22

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GTTACTAACG GAACGAGACC TA

22

(2) INFORMATION FOR SEQ ID NO:153:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

TGTTGGCGTT CTCAACCCCG TT

22

15 (2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

ACAACCGGAG TTGTTCTGCC TA

22

(2) INFORMATION FOR SEQ ID NO:155:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

TAAGCATCGG CCACGTTCTT CG

22

(2) INFORMATION FOR SEQ ID NO:156:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

TTATCCCTGG TGTGCAGGTT GA 22

5 (2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

TATCAGAAC TGTAGTCGGAC GG 22

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

CTTTGTAATG GAACCACAAAC CC 22

(2) INFORMATION FOR SEQ ID NO:159:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

25 CGGTGGCTCA TCTCCCTCTT AT 22

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:
ATCAGACTGG CTGGGACCA AA 22

(2) INFORMATION FOR SEQ ID NO:161:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:
CACAAACCTCC TCTCCGCGAA CT 22

10 (2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:
AGATTCTGCC CCAACGCGTG AT 22

(2) INFORMATION FOR SEQ ID NO:163:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:
GGGAATTCTGC AAAGCTATAAC TC 22

(2) INFORMATION FOR SEQ ID NO:164:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:
CCCCGTGGAA TTCAACCTGT GA 22

30 (2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

GTCGTCTTTC CAGACGT

17

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

CTTGCATGCC TGCAGGTCGA C

21

(2) INFORMATION FOR SEQ ID NO:167:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

20 Arg Ile Ala Gly Leu Pro Trp Tyr Arg Cys Arg Thr Val Ala Phe Glu
1 5 10 15
Thr Gly Met Gln Asn Thr Gln Leu Cys Ser Thr Ile Val Gln Leu Ser
20 25 30
Phe Thr Pro Glu Glu
35

(2) INFORMATION FOR SEQ ID NO:168:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

30 Arg Glu Phe Ala Glu Arg Arg Leu Trp Gly Cys Asp Asp Leu Ser Trp
1 5 10 15
Arg Leu Asp Ala Glu Gly Cys Gly Pro Thr Pro Ser Asn Arg Ala Val
20 25 30

Lys His Arg Lys Pro Arg Pro Arg Ser Pro Ala Leu
35 40

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

5

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

Ser Gly Ser His Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val Phe
1 5 10 15
Arg Glu Leu Arg Asp Arg Trp Tyr Ala Thr Ser His His Thr Arg Pro
10 20 25 30
Thr Pro Gln Leu Pro Arg Gly Pro Asn
35 40

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

15

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp
1 5 10 15
Ser Asp Ser Asp
20

20

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp
1 5 10 15
Ser Asp Ser Asp Thr Asn Ala Lys His Ser Ser His Asn
20 25

(2) INFORMATION FOR SEQ ID NO:172:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

5 Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg Ser
1 5 10 15
Arg Pro Asn

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

10 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

Thr Asn Ala Lys His Ser Ser His Asn
1 5

(2) INFORMATION FOR SEQ ID NO:174:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

20 Ser Ser His Asn Arg Arg Leu Arg Thr Arg Ser Arg Pro Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

25 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

Arg Arg Leu Arg Thr Arg Ser Arg Pro Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:176:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 708 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

5	Met Gly Met Ser Lys Ser His Ser Phe Phe Gly Tyr Pro Leu Ser Ile	
	1 5 10 15	
	Phe Phe Ile Val Val Asn Glu Phe Cys Glu Arg Phe Ser Tyr Tyr Gly	
	20 25 30	
	Met Arg Ala Ile Leu Ile Leu Tyr Phe Thr Asn Phe Ile Ser Trp Asp	
	35 40 45	
	Asp Asn Leu Ser Thr Ala Ile Tyr His Thr Phe Val Ala Leu Cys Tyr	
	50 55 60	
	Leu Thr Pro Ile Leu Gly Ala Leu Ile Ala Asp Ser Trp Leu Gly Lys	
	65 70 75 80	
10	Phe Lys Thr Ile Val Ser Leu Ser Ile Val Tyr Thr Ile Gly Gln Ala	
	85 90 95	
	Val Thr Ser Val Ser Ser Ile Asn Asp Leu Thr Asp His Asn His Asp	
	100 105 110	
	Gly Thr Pro Asp Ser Leu Pro Val His Val Val Leu Ser Leu Ile Gly	
	115 120 125	
	Leu Ala Leu Ile Ala Leu Gly Thr Gly Gly Ile Lys Pro Cys Val Ser	
	130 135 140	
	Ala Phe Gly Gly Asp Gln Phe Glu Glu Gly Gln Glu Lys Gln Arg Asn	
	145 150 155 160	
15	Arg Phe Phe Ser Ile Phe Tyr Leu Ala Ile Asn Ala Gly Ser Leu Leu	
	165 170 175	
	Ser Thr Ile Ile Thr Pro Met Leu Arg Val Gln Gln Cys Gly Ile His	
	180 185 190	
	Ser Lys Gln Ala Cys Tyr Pro Leu Ala Phe Gly Val Pro Ala Ala Leu	
	195 200 205	
	Met Ala Val Ala Leu Ile Val Phe Val Leu Gly Ser Gly Met Tyr Lys	
	210 215 220	
	Lys Phe Lys Pro Gln Gly Asn Ile Met Gly Lys Val Ala Lys Cys Ile	
	225 230 235 240	
20	Gly Phe Ala Ile Lys Asn Arg Phe Arg His Arg Ser Lys Ala Phe Pro	
	245 250 255	
	Lys Arg Glu His Trp Leu Asp Trp Ala Lys Glu Lys Tyr Asp Glu Arg	
	260 265 270	
	Leu Ile Ser Gln Ile Lys Met Val Thr Arg Val Met Phe Leu Tyr Ile	
	275 280 285	
	Pro Leu Pro Met Phe Trp Ala Leu Phe Asp Gln Gln Gly Ser Arg Trp	
	290 295 300	
	Thr Leu Gln Ala Thr Thr Met Ser Gly Lys Ile Gly Ala Leu Glu Ile	
	305 310 315 320	
25	Gln Pro Asp Gln Met Gln Thr Val Asn Ala Ile Leu Ile Val Ile Met	
	325 330 335	
	Val Pro Ile Phe Asp Ala Val Leu Tyr Pro Leu Ile Ala Lys Cys Gly	
	340 345 350	
	Phe Asn Phe Thr Ser Leu Lys Lys Met Ala Val Gly Met Val Leu Ala	
	355 360 365	
	Ser Met Ala Phe Val Val Ala Ala Ile Val Gln Val Glu Ile Asp Lys	
	370 375 380	
	Thr Leu Pro Val Phe Pro Lys Gly Asn Glu Val Gln Ile Lys Val Leu	
	385 390 395 400	
30	Asn Ile Gly Asn Asn Thr Met Asn Ile Ser Leu Pro Gly Glu Met Val	
	405 410 415	
	Thr Leu Gly Pro Met Ser Gln Thr Asn Ala Phe Met Thr Phe Asp Val	

	420	425	430
	Asn Lys Leu Thr Arg Ile Asn Ile Ser Ser Pro Gly Ser Pro Val Thr		
	435	440	445
	Ala Val Thr Asp Asp Phe Lys Gln Gly Gln Arg His Thr Leu Leu Val		
	450	455	460
	Trp Ala Pro Asn His Tyr Gln Val Val Lys Asp Gly Leu Asn Gln Lys		
	465	470	475
	Pro Glu Lys Gly Glu Asn Gly Ile Arg Phe Val Asn Thr Phe Asn Glu		
5	485	490	495
	Leu Ile Thr Ile Thr Met Ser Gly Lys Val Tyr Ala Asn Ile Ser Ser		
	500	505	510
	Tyr Asn Ala Ser Thr Tyr Gln Phe Phe Pro Ser Gly Ile Lys Gly Phe		
	515	520	525
	Thr Ile Ser Ser Thr Glu Ile Pro Pro Gln Cys Gln Pro Asn Phe Asn		
	530	535	540
	Thr Phe Tyr Leu Glu Phe Gly Ser Ala Tyr Thr Tyr Ile Val Gln Arg		
	545	550	555
	Lys Asn Asp Ser Cys Pro Glu Val Lys Val Phe Glu Asp Ile Ser Ala		
10	565	570	575
	Asn Thr Val Asn Met Ala Leu Gln Ile Pro Gln Tyr Phe Leu Leu Thr		
	580	585	590
	Cys Gly Glu Val Val Phe Ser Val Thr Gly Leu Glu Phe Ser Tyr Ser		
	595	600	605
	Gln Ala Pro Ser Asn Met Lys Ser Val Leu Gln Ala Gly Trp Leu Leu		
	610	615	620
	Thr Val Ala Val Gly Asn Ile Ile Val Leu Ile Val Ala Gly Ala Gly		
	625	630	635
	Gln Phe Ser Lys Gln Trp Ala Glu Tyr Ile Leu Phe Ala Ala Leu Leu		
15	645	650	655
	Leu Val Val Cys Val Val Phe Ala Ile Met Ala Arg Phe Tyr Thr Tyr		
	660	665	670
	Ile Asn Pro Ala Glu Ile Glu Ala Gln Phe Asp Glu Asp Glu Lys Lys		
	675	680	685
	Asn Arg Leu Glu Lys Ser Asn Pro Tyr Phe Met Ser Gly Ala Asn Ser		
	690	695	700
	Gln Lys Gln Met		
	705		

20 (2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA
- (ix) FEATURE:

- 25 (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 88...2583
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GAATTCCGTC TCGACCCTG AATGGAAGAA AAGGACTTTT AACCACCAT TTGTGACTTA	60
CAGAAAGGAA TTTGAATAAA GAAAACT ATG ATA CTT CAG GCC CAT CTT CAC TCC	114
Met Ile Leu Gln Ala His Leu His Ser	
30 1	5

	CTG TGT CTT CTT ATG CTT TAT TTG GCA ACT GGA TAT GGC CAA GAG GGG Leu Cys Leu Leu Met Leu Tyr Leu Ala Thr Gly Tyr Gly Gln Glu Gly 10 15 20 25	162
	AAG TTT AGT GGA CCC CTG AAA CCC ATG ACA TTT TCT ATT TAT GAA GGC Lys Phe Ser Gly Pro Leu Lys Pro Met Thr Phe Ser Ile Tyr Glu Gly 30 35 40	210
5	CAA GAA CCG AGT CAA ATT ATA TTC CAG TTT AAG GCC AAT CCT CCT GCT Gln Glu Pro Ser Gln Ile Ile Phe Gln Phe Lys Ala Asn Pro Pro Ala 45 50 55	258
	GTG ACT TTT GAA CTA ACT GGG GAG ACA GAC AAC ATA TTT GTG ATA GAA Val Thr Phe Glu Leu Thr Gly Glu Thr Asp Asn Ile Phe Val Ile Glu 60 65 70	306
10	CGG GAG GGA CTT CTG TAT TAC AAC AGA GCC TTG GAC AGG GAA ACA AGA Arg Glu Gly Leu Leu Tyr Tyr Asn Arg Ala Leu Asp Arg Glu Thr Arg 75 80 85	354
	TCT ACT CAC AAT CTC CAG GTT GCA GCC CTG GAC GCT AAT GGA ATT ATA Ser Thr His Asn Leu Gln Val Ala Ala Leu Asp Ala Asn Gly Ile Ile 90 95 100 105	402
	GTG GAG GGT CCA GTC CCT ATC ACC ATA GAA GTG AAG GAC ATC AAC GAC Val Glu Gly Pro Val Pro Ile Thr Ile Glu Val Lys Asp Ile Asn Asp 110 115 120	450
15	AAT CGA CCC ACG TTT CTC CAG TCA AAG TAC GAA GGC TCA GTA AGG CAG Asn Arg Pro Thr Phe Leu Gln Ser Lys Tyr Glu Gly Ser Val Arg Gln 125 130 135	498
	AAC TCT CGC CCA GGA AAG CCC TTC TTG TAT GTC AAT GCC ACA GAC CTG Asn Ser Arg Pro Gly Lys Pro Phe Leu Tyr Val Asn Ala Thr Asp Leu 140 145 150	546
20	GAT GAT CCG GCC ACT CCC AAT GGC CAG CTT TAT TAC CAG ATT GTC ATC Asp Asp Pro Ala Thr Pro Asn Gly Gln Leu Tyr Tyr Gln Ile Val Ile 155 160 165	594
	CAG CTT CCC ATG ATC AAC AAT GTC ATG TAC TTT CAG ATC AAC AAC AAA Gln Leu Pro Met Ile Asn Asn Val Met Tyr Phe Gln Ile Asn Asn Lys 170 175 180 185	642
	ACG GGA GCC ATC TCT CTT ACC CGA GAG GGA TCT CAG GAA TTG AAT CCT Thr Gly Ala Ile Ser Leu Thr Arg Glu Gly Ser Gln Glu Leu Asn Pro 190 195 200	690
25	GCT AAG AAT CCT TCC TAT AAT CTG GTG ATC TCA GTG AAG GAC ATG GGA Ala Lys Asn Pro Ser Tyr Asn Leu Val Ile Ser Val Lys Asp Met Gly 205 210 215	738
	GGC CAG AGT GAG AAT TCC TTC AGT GAT ACC ACA TCT GTG GAT ATC ATA Gly Gln Ser Glu Asn Ser Phe Ser Asp Thr Thr Ser Val Asp Ile Ile 220 225 230	786
	GTG ACA GAG AAT ATT TGG AAA GCA CCA AAA CCT GTG GAG ATG GTG GAA Val Thr Glu Asn Ile Trp Lys Ala Pro Lys Pro Val Glu Met Val Glu 235 240 245	834
30	AAC TCA ACT GAT CCT CAC CCC ATC AAA ATC ACT CAG GTG CGG TGG AAT	882

	Asn Ser Thr Asp Pro His Pro Ile Lys Ile Thr Gln Val Arg Trp Asn	250	255	260	265	
	GAT CCC GGT GCA CAA TAT TCC TTA GTT GAC AAA GAG AAG CTG CCA AGA					930
	Asp Pro Gly Ala Gln Tyr Ser Leu Val Asp Lys Glu Lys Leu Pro Arg	270	275		280	
5	TTC CCA TTT TCA ATT GAC CAG GAA GGA GAT ATT TAC GTG ACT CAG CCC					978
	Phe Pro Phe Ser Ile Asp Gln Glu Gly Asp Ile Tyr Val Thr Gln Pro	285	290		295	
	TTG GAC CGA GAA GAA AAG GAT GCA TAT GTT TTT TAT GCA GTT GCA AAG					1026
	Leu Asp Arg Glu Glu Lys Asp Ala Tyr Val Phe Tyr Ala Val Ala Lys	300	305		310	
	GAT GAG TAC GGA AAA CCA CTT TCA TAT CCG CTG GAA ATT CAT GTA AAA					1074
	Asp Glu Tyr Gly Lys Pro Leu Ser Tyr Pro Leu Glu Ile His Val Lys	315	320		325	
10	GTT AAA GAT ATT AAT GAT AAT CCA CCT ACA TGT CCG TCA CCA GTA ACC					1122
	Val Lys Asp Ile Asn Asp Asn Pro Pro Thr Cys Pro Ser Pro Val Thr	330	335		340	
	GTA TTT GAG GTC CAG GAG AAT GAA CGA CTG GGT AAC AGT ATC GGG ACC					1170
	Val Phe Glu Val Gln Glu Asn Glu Arg Leu Gly Asn Ser Ile Gly Thr	350	355		360	
15	CTT ACT GCA CAT GAC AGG GAT GAA GAA AAT ACT GCC AAC AGT TTT CTA					1218
	Leu Thr Ala His Asp Arg Asp Glu Glu Asn Thr Ala Asn Ser Phe Leu	365	370		375	
	AAC TAC AGG ATT GTG GAG CAA ACT CCC AAA CTT CCC ATG GAT GGA CTC					1266
	Asn Tyr Arg Ile Val Glu Gln Thr Pro Lys Leu Pro Met Asp Gly Leu	380	385		390	
	TTC CTA ATC CAA ACC TAT GCT GGA ATG TTA CAG TTA GCT AAA CAG TCC					1314
	Phe Leu Ile Gln Thr Tyr Ala Gly Met Leu Gln Leu Ala Lys Gln Ser	395	400		405	
20	TTG AAG AAG CAA GAT ACT CCT CAG TAC AAC TTA ACG ATA GAG GTG TCT					1362
	Leu Lys Lys Gln Asp Thr Pro Gln Tyr Asn Leu Thr Ile Glu Val Ser	410	415		420	
	425					
	GAC AAA GAT TTC AAG ACC CTT TGT TTT GTG CAA ATC AAC GTT ATT GAT					1410
	Asp Lys Asp Phe Lys Thr Leu Cys Phe Val Gln Ile Asn Val Ile Asp	430	435		440	
	ATC AAT GAT CAG ATC CCC ATC TTT GAA AAA TCA GAT TAT GGA AAC CTG					1458
25	Ile Asn Asp Gln Ile Pro Ile Phe Glu Lys Ser Asp Tyr Gly Asn Leu	445	450		455	
	455					
	ACT CTT GCT GAA GAC ACA AAC ATT GGG TCC ACC ATC TTA ACC ATC CAG					1506
	Thr Leu Ala Glu Asp Thr Asn Ile Gly Ser Thr Ile Leu Thr Ile Gln	460	465		470	
	470					
	GCC ACT GAT GCT GAT GAG CCA TTT ACT GGG AGT TCT AAA ATT CTG TAT					1554
	Ala Thr Asp Ala Asp Glu Pro Phe Thr Gly Ser Ser Lys Ile Leu Tyr	475	480		485	
30	CAT ATC ATA AAG GGA GAC AGT GAG GGA CGC CTG GGG GTT GAC ACA GAT					1602
	His Ile Ile Lys Gly Asp Ser Glu Gly Arg Leu Gly Val Asp Thr Asp					

	490	495	500	505	
	CCC CAT ACC AAC ACC GGA TAT GTC ATA ATT AAA AAG CCT CTT GAT TTT Pro His Thr Asn Thr Gly Tyr Val Ile Ile Lys Lys Pro Leu Asp Phe 510		515		1650
	GAA ACA GCA GCT GTT TCC AAC ATT GTG TTC AAA GCA GAA AAT CCT GAG Glu Thr Ala Ala Val Ser Asn Ile Val Phe Lys Ala Glu Asn Pro Glu 5 525		530		1698
	CCT CTA GTG TTT GGT GTG AAG TAC AAT GCA AGT TCT TTT GCC AAG TTC Pro Leu Val Phe Gly Val Lys Tyr Asn Ala Ser Ser Phe Ala Lys Phe 540		545		1746
	ACG CTT ATT GTG ACA GAT GTG AAT GAA GCA CCT CAA TTT TCC CAA CAC Thr Leu Ile Val Thr Asp Val Asn Glu Ala Pro Gln Phe Ser Gln His 555		560		1794
10	GTA TTC CAA GCG AAA GTC AGT GAG GAT GTA GCT ATA GGC ACT AAA GTG Val Phe Gln Ala Lys Val Ser Glu Asp Val Ala Ile Gly Thr Lys Val 570		575		1842
	GGC AAT GTG ACT GCC AAG GAT CCA GAA GGT CTG GAC ATA AGC TAT TCA Gly Asn Val Thr Ala Lys Asp Pro Glu Gly Leu Asp Ile Ser Tyr Ser 590		595		1890
	CTG AGG GGA GAC ACA AGA GGT TGG CTT AAA ATT GAC CAC GTG ACT GGT Leu Arg Gly Asp Thr Arg Gly Trp Leu Lys Ile Asp His Val Thr Gly 15 605		610		1938
	GAG ATC TTT AGT GTG GCT CCA TTG GAC AGA GAA GCC GGA AGT CCA TAT Glu Ile Phe Ser Val Ala Pro Leu Asp Arg Glu Ala Gly Ser Pro Tyr 620		625		1986
	CGG GTA CAA GTG GTG GCC ACA GAA GTA GGG GGG TCT TCC TTA AGC TCT Arg Val Gln Val Val Ala Thr Glu Val Gly Gly Ser Ser Leu Ser Ser 635		640		2034
20	GTG TCA GAG TTC CAC CTG ATC CTT ATG GAT GTG AAT GAC AAC CCT CCC Val Ser Glu Phe His Leu Ile Leu Met Asp Val Asn Asp Asn Pro Pro 650		655		2082
	AGG CTA GCC AAG GAC TAC ACG GGC TTG TTC TGC CAT CCC CTC AGT Arg Leu Ala Lys Asp Tyr Thr Gly Leu Phe Phe Cys His Pro Leu Ser 670		675		2130
	GCA CCT GGA AGT CTC ATT TTC GAG GCT ACT GAT GAT GAT CAG CAC TTA Ala Pro Gly Ser Leu Ile Phe Glu Ala Thr Asp Asp Asp Gln His Leu 25 685		690		2178
	TTT CGG GGT CCC CAT TTT ACA TTT TCC CTC GGC AGT GGA AGC TTA CAA Phe Arg Gly Pro His Phe Thr Phe Ser Leu Gly Ser Gly Ser Leu Gln 700		705		2226
	AAC GAC TGG GAA GTT TCC AAA ATC AAT GGT ACT CAT GCC CGA CTG TCT Asn Asp Trp Glu Val Ser Lys Ile Asn Gly Thr His Ala Arg Leu Ser 715		720		2274
30	ACC AGG CAC ACA GAC TTT GAG GAG AGG GCG TAT GTC GTC TTG ATC CGC Thr Arg His Thr Asp Phe Glu Glu Arg Ala Tyr Val Val Leu Ile Arg 730		735		2322
			740		745

	ATC AAT GAT GGG GGT CGG CCA CCC TTG GAA GGC ATT GTT TCT TTA CCA Ile Asn Asp Gly Gly Arg Pro Pro Leu Glu Gly Ile Val Ser Leu Pro 750 755 760	2370
	GTT ACA TTC TGC AGT TGT GTG GAA GGA AGT TGT TTC CGG CCA GCA GGT Val Thr Phe Cys Ser Cys Val Glu Gly Ser Cys Phe Arg Pro Ala Gly 765 770 775	2418
5	CAC CAG ACT GGG ATA CCC ACT GTG GGC ATG GCA GTT GGT ATA CTG CTG His Gln Thr Gly Ile Pro Thr Val Gly Met Ala Val Gly Ile Leu Leu 780 785 790	2466
	ACC ACC CTT CTG GTG ATT GGT ATA ATT TTA GCA GTT GTG TTT ATC CGC Thr Thr Leu Leu Val Ile Gly Ile Ile Leu Ala Val Val Phe Ile Arg 795 800 805	2514
10	ATA AAG AAG GAT AAA GGC AAA GAT AAT GTT GAA AGT GCT CAA GCA TCT Ile Lys Lys Asp Lys Gly Lys Asp Asn Val Glu Ser Ala Gln Ala Ser 810 815 820 825	2562
	GAA GTC AAA CCT CTG AGA AGC TGAATTGAA AAGGAATGTT TGAATTATA TAGC Glu Val Lys Pro Leu Arg Ser 830	2617
15	AAGTGCTATT TCAGCAACAA CCATCTCATC CTATTACTTT TCATCTAACG TGCAATTATAA TTTTTAAAC AGATATCCC TCTTGTCCCT TAATATTGCG TAAATATTTC TTTTTGAGG TGGAGTCTTG CTCTGTCGCC CAGGCTGGAG TACAGTGGTG TGATCCCAGC TCACTGCAAC CTCCGCCTCC TGGGTTCACTA TGATTCTCCT GCCTCAGCTT CCTAAGTAGC TGGGTTTACA GGCACCCACC ACCATGCCCA GCTAATTCTT GTATTCTTAA TAGAGACGGG GTTTCGCCAT TTGGCCAGGC TGGTCTGAA CTCCTGACGT CAAGTGATCT GCCTGCCTG GTCTCCCAAT ACAGGCATGA ACCACTGCAC CCACCTACTT AGATATTCA TGTGCTATAG ACATTAGAGA GATTTTCAT TTTCCATGA CATTTCCT CTCTGCAAAT GGCTTAGCTA CTTGTGTTTT TCCCTTTGG GGCAAGACAG ACTCATTAAA TATTCTGTAC ATTTTTCTT TATCAAGGAG ATATATCAGT GTTGTCTCAT AGAACTGCCT GGATTCCATT TATGTTTTT CTGATTCCAT CCTGTGTCCC CTTCATCCTT GACTCCTTTG GTATTCACT GAATTTCAA CATTGTCAG AGAAGAAAAA AGTGAGGACT CAGGAAAAAT AAATAAATAA AAGAACAGCC TTTTGCAGGC GCGAATTC	2677 2737 2797 2857 2917 2977 3037 3097 3157 3217 3277 3337 3345

20 (2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 832 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

	Met Ile Leu Gln Ala His Leu His Ser Leu Cys Leu Leu Met Leu Tyr 1 5 10 15
	Leu Ala Thr Gly Tyr Gly Gln Glu Gly Lys Phe Ser Gly Pro Leu Lys 20 25 30
	Pro Met Thr Phe Ser Ile Tyr Glu Gly Gln Glu Pro Ser Gln Ile Ile 35 40 45
	Phe Gln Phe Lys Ala Asn Pro Pro Ala Val Thr Phe Glu Leu Thr Gly 50 55 60
30	Glu Thr Asp Asn Ile Phe Val Ile Glu Arg Glu Gly Leu Leu Tyr Tyr 65 70 75 80
	Asn Arg Ala Leu Asp Arg Glu Thr Arg Ser Thr His Asn Leu Gln Val

	85	90	95
	Ala Ala Leu Asp Ala Asn Gly Ile Ile Val Glu Gly Pro Val Pro Ile		
	100	105	110
	Thr Ile Glu Val Lys Asp Ile Asn Asp Asn Arg Pro Thr Phe Leu Gln		
	115	120	125
	Ser Lys Tyr Glu Gly Ser Val Arg Gln Asn Ser Arg Pro Gly Lys Pro		
	130	135	140
5	Phe Leu Tyr Val Asn Ala Thr Asp Leu Asp Asp Pro Ala Thr Pro Asn		
	145	150	155
	Gly Gln Leu Tyr Gln Ile Val Ile Gln Leu Pro Met Ile Asn Asn		
	165	170	175
	Val Met Tyr Phe Gln Ile Asn Asn Lys Thr Gly Ala Ile Ser Leu Thr		
	180	185	190
	Arg Glu Gly Ser Gln Glu Leu Asn Pro Ala Lys Asn Pro Ser Tyr Asn		
	195	200	205
	Leu Val Ile Ser Val Lys Asp Met Gly Gly Gln Ser Glu Asn Ser Phe		
	210	215	220
10	Ser Asp Thr Thr Ser Val Asp Ile Ile Val Thr Glu Asn Ile Trp Lys		
	225	230	235
	Ala Pro Lys Pro Val Glu Met Val Glu Asn Ser Thr Asp Pro His Pro		
	245	250	255
	Ile Lys Ile Thr Gln Val Arg Trp Asn Asp Pro Gly Ala Gln Tyr Ser		
	260	265	270
	Leu Val Asp Lys Glu Lys Leu Pro Arg Phe Pro Phe Ser Ile Asp Gln		
	275	280	285
	Glu Gly Asp Ile Tyr Val Thr Gln Pro Leu Asp Arg Glu Glu Lys Asp		
	290	295	300
15	Ala Tyr Val Phe Tyr Ala Val Ala Lys Asp Glu Tyr Gly Lys Pro Leu		
	305	310	315
	Ser Tyr Pro Leu Glu Ile His Val Lys Val Lys Asp Ile Asn Asp Asn		
	325	330	335
	Pro Pro Thr Cys Pro Ser Pro Val Thr Val Phe Glu Val Gln Glu Asn		
	340	345	350
	Glu Arg Leu Gly Asn Ser Ile Gly Thr Leu Thr Ala His Asp Arg Asp		
	355	360	365
	Glu Glu Asn Thr Ala Asn Ser Phe Leu Asn Tyr Arg Ile Val Glu Gln		
	370	375	380
20	Thr Pro Lys Leu Pro Met Asp Gly Leu Phe Leu Ile Gln Thr Tyr Ala		
	385	390	395
	Gly Met Leu Gln Leu Ala Lys Gln Ser Leu Lys Lys Gln Asp Thr Pro		
	405	410	415
	Gln Tyr Asn Leu Thr Ile Glu Val Ser Asp Lys Asp Phe Lys Thr Leu		
	420	425	430
	Cys Phe Val Gln Ile Asn Val Ile Asp Ile Asn Asp Gln Ile Pro Ile		
	435	440	445
	Phe Glu Lys Ser Asp Tyr Gly Asn Leu Thr Leu Ala Glu Asp Thr Asn		
	450	455	460
25	Ile Gly Ser Thr Ile Leu Thr Ile Gln Ala Thr Asp Ala Asp Glu Pro		
	465	470	475
	Phe Thr Gly Ser Ser Lys Ile Leu Tyr His Ile Ile Lys Gly Asp Ser		
	485	490	495
	Glu Gly Arg Leu Gly Val Asp Thr Asp Pro His Thr Asn Thr Gly Tyr		
	500	505	510
	Val Ile Ile Lys Lys Pro Leu Asp Phe Glu Thr Ala Ala Val Ser Asn		
	515	520	525
	Ile Val Phe Lys Ala Glu Asn Pro Glu Pro Leu Val Phe Gly Val Lys		
	530	535	540
30	Tyr Asn Ala Ser Ser Phe Ala Lys Phe Thr Leu Ile Val Thr Asp Val		
	545	550	555
	Asn Glu Ala Pro Gln Phe Ser Gln His Val Phe Gln Ala Lys Val Ser		
	565	570	575

	Glu	Asp	Val	Ala	Ile	Gly	Thr	Lys	Val	Gly	Asn	Val	Thr	Ala	Lys	Asp	
															590		
	580							585									
	Pro	Glu	Gly	Leu	Asp	Ile	Ser	Tyr	Ser	Leu	Arg	Gly	Asp	Thr	Arg	Gly	
															605		
	595							600									
	Trp	Leu	Lys	Ile	Asp	His	Val	Thr	Gly	Glu	Ile	Phe	Ser	Val	Ala	Pro	
															620		
	610							615									
	Leu	Asp	Arg	Glu	Ala	Gly	Ser	Pro	Tyr	Arg	Val	Gln	Val	Val	Ala	Thr	
															640		
	625							630				635					
5	Glu	Val	Gly	Gly	Ser	Ser	Leu	Ser	Ser	Val	Ser	Glu	Phe	His	Leu	Ile	
															655		
												645		650			
	645																
	Leu	Met	Asp	Val	Asn	Asp	Asn	Pro	Pro	Arg	Leu	Ala	Lys	Asp	Tyr	Thr	
															670		
												660		665			
	660																
	Gly	Leu	Phe	Phe	Cys	His	Pro	Leu	Ser	Ala	Pro	Gly	Ser	Leu	Ile	Phe	
															685		
												675		680			
	675																
	Glu	Ala	Thr	Asp	Asp	Asp	Gln	His	Leu	Phe	Arg	Gly	Pro	His	Phe	Thr	
															700		
												690		695			
	690																
	Phe	Ser	Leu	Gly	Ser	Gly	Ser	Leu	Gln	Asn	Asp	Trp	Glu	Val	Ser	Lys	
															720		
												705		710			
10	Ile	Asn	Gly	Thr	His	Ala	Arg	Leu	Ser	Thr	Arg	His	Thr	Asp	Phe	Glu	
															735		
												725		730			
	725																
	Glu	Arg	Ala	Tyr	Val	Val	Leu	Ile	Arg	Ile	Asn	Asp	Gly	Gly	Arg	Pro	
															750		
												740		745			
	740																
	Pro	Leu	Glu	Gly	Ile	Val	Ser	Leu	Pro	Val	Thr	Phe	Cys	Ser	Cys	Val	
															765		
												755		760			
	755																
	Glu	Gly	Ser	Cys	Phe	Arg	Pro	Ala	Gly	His	Gln	Thr	Gly	Ile	Pro	Thr	
															780		
												770		775			
	770																
	Val	Gly	Met	Ala	Val	Gly	Ile	Leu	Leu	Thr	Thr	Leu	Leu	Val	Ile	Gly	
															800		
												785		790			
15	Ile	Ile	Leu	Ala	Val	Val	Phe	Ile	Arg	Ile	Lys	Lys	Asp	Lys	Gly	Lys	
															815		
												805		810			
	805																
	Asp	Asn	Val	Glu	Ser	Ala	Gln	Ala	Ser	Glu	Val	Lys	Pro	Leu	Arg	Ser	
															830		
												820		825			

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1827 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

	Met	Ala	Arg	Lys	Lys	Phe	Ser	Gly	Leu	Glu	Ile	Ser	Leu	Ile	Val	Leu	
	1															15	
	5																
	Pro	Val	Ile	Val	Thr	Ile	Ile	Ala	Ile	Ala	Leu	Ile	Val	Val	Leu	Ala	
															30		
25																	
	20																
	Thr	Lys	Thr	Pro	Ala	Val	Asp	Glu	Ile	Ser	Asp	Ser	Thr	Ser	Thr	Pro	
															45		
	35																
	Ala	Thr	Thr	Arg	Val	Thr	Thr	Asn	Pro	Ser	Asp	Ser	Gly	Lys	Cys	Pro	
															60		
												50		55			
	50																
	Asn	Val	Leu	Asn	Asp	Pro	Val	Asn	Val	Arg	Ile	Asn	Cys	Ile	Pro	Glu	
															80		
	65																
	70																
	Gln	Phe	Pro	Thr	Glu	Gly	Ile	Cys	Ala	Gln	Arg	Gly	Cys	Cys	Trp	Arg	
															95		
												85		90			
	85																
	Pro	Trp	Asn	Asp	Ser	Leu	Ile	Pro	Trp	Cys	Phe	Phe	Val	Asp	Asn	His	
															110		
												100		105			
30																	
	Gly	Tyr	Asn	Val	Gln	Asp	Met	Thr	Thr	Thr	Ser	Ile	Gly	Val	Glu	Ala	
															125		
												115		120			

Lys Leu Asn Arg Ile Pro Ser Pro Thr Leu Phe Gly Asn Asp Ile Asn
 130 135 140
 Ser Val Leu Phe Thr Thr Gln Asn Gln Thr Pro Asn Arg Phe Arg Phe
 145 150 155 160
 Lys Ile Thr Asp Pro Asn Asn Arg Arg Tyr Glu Val Pro His Gln Tyr
 165 170 175
 Val Lys Glu Phe Thr Gly Pro Thr Val Ser Asp Thr Leu Tyr Asp Val
 180 185 190
5 Lys Val Ala Gln Asn Pro Phe Ser Ile Gln Val Ile Arg Lys Ser Asn
 195 200 205
 Gly Lys Thr Leu Phe Asp Thr Ser Ile Gly Pro Leu Val Tyr Ser Asp
 210 215 220
 Gln Tyr Leu Gln Ile Ser Ala Arg Leu Pro Ser Asp Tyr Ile Tyr Gly
 225 230 235 240
 Ile Gly Glu Gln Val His Lys Arg Phe Arg His Asp Leu Ser Trp Lys
 245 250 255
 Thr Trp Pro Ile Phe Thr Arg Asp Gln Leu Pro Gly Asp Asn Asn Asn
 260 265 270
10 Asn Leu Tyr Gly His Gln Thr Phe Phe Met Cys Ile Glu Asp Thr Ser
 275 280 285
 Gly Lys Ser Phe Gly Val Phe Leu Met Asn Ser Asn Ala Met Glu Ile
 290 295 300
 Phe Ile Gln Pro Thr Pro Ile Val Thr Tyr Arg Val Thr Gly Gly Ile
 305 310 315 320
 Leu Asp Phe Tyr Ile Leu Leu Gly Asp Thr Pro Glu Gln Val Val Gln
 325 330 335
 Gln Tyr Gln Gln Leu Val Gly Leu Pro Ala Met Pro Ala Tyr Trp Asn
 340 345 350
15 Leu Gly Phe Gln Leu Ser Arg Trp Asn Tyr Lys Ser Leu Asp Val Val
 355 360 365
 Lys Glu Val Val Arg Arg Asn Arg Glu Ala Gly Ile Pro Phe Asp Thr
 370 375 380
 Gln Val Thr Asp Ile Asp Tyr Met Glu Asp Lys Lys Asp Phe Thr Tyr
 385 390 395 400
 Asp Gln Val Ala Phe Asn Gly Leu Pro Gln Phe Val Gln Asp Leu His
 405 410 415
 Asp His Gly Gln Lys Tyr Val Ile Ile Leu Asp Pro Ala Ile Ser Ile
 420 425 430
20 Gly Arg Arg Ala Asn Gly Thr Thr Tyr Ala Thr Tyr Glu Arg Gly Asn
 435 440 445
 Thr Gln His Val Trp Ile Asn Glu Ser Asp Gly Ser Thr Pro Ile Ile
 450 455 460
 Gly Glu Val Trp Pro Gly Leu Thr Val Tyr Pro Asp Phe Thr Asn Pro
 465 470 475 480
 Asn Cys Ile Asp Trp Trp Ala Asn Glu Cys Ser Ile Phe His Gln Glu
 485 490 495
 Val Gln Tyr Asp Gly Leu Trp Ile Asp Met Asn Glu Val Ser Ser Phe
 500 505 510
25 Ile Gln Gly Ser Thr Lys Gly Cys Asn Val Asn Lys Leu Asn Tyr Pro
 515 520 525
 Pro Phe Thr Pro Asp Ile Leu Asp Lys Leu Met Tyr Ser Lys Thr Ile
 530 535 540
 Cys Met Asp Ala Val Gln Asn Trp Gly Lys Gln Tyr Asp Val His Ser
 545 550 555 560
 Leu Tyr Gly Tyr Ser Met Ala Ile Ala Thr Glu Gln Ala Val Gln Lys
 565 570 575
 Val Phe Pro Asn Lys Arg Ser Phe Ile Leu Thr Arg Ser Thr Phe Ala
 580 585 590
30 Gly Ser Gly Arg His Ala Ala His Trp Leu Gly Asp Asn Thr Ala Ser
 595 600 605
 Trp Glu Gln Met Glu Trp Ser Ile Thr Gly Met Leu Glu Phe Ser Leu

	610	615	620													
	Phe	Gly	Ile	Pro	Leu	Val	Gly	Ala	Asp	Ile	Cys	Gly	Phe	Val	Ala	Glu
	625	630	635	640												
	Thr	Thr	Glu	Glu	Leu	Cys	Arg	Arg	Trp	Met	Gln	Leu	Gly	Ala	Phe	Tyr
	645	650	655	655												
	Pro	Phe	Ser	Arg	Asn	His	Asn	Ser	Asp	Gly	Tyr	Glu	His	Gln	Asp	Pro
	660	665	670	670												
	Ala	Phe	Phe	Gly	Gln	Asn	Ser	Leu	Leu	Val	Lys	Ser	Ser	Arg	Gln	Tyr
5	675	680	685	685												
	Leu	Thr	Ile	Arg	Tyr	Thr	Leu	Leu	Pro	Phe	Leu	Tyr	Thr	Leu	Phe	Tyr
	690	695	700	700												
	Lys	Ala	His	Val	Phe	Gly	Glu	Thr	Val	Ala	Arg	Pro	Val	Leu	His	Glu
	705	710	715	720												
	Phe	Tyr	Glu	Asp	Thr	Asn	Ser	Trp	Ile	Glu	Asp	Thr	Glu	Phe	Leu	Trp
	725	730	735	735												
	Gly	Pro	Ala	Leu	Leu	Ile	Thr	Pro	Val	Leu	Lys	Gln	Gly	Ala	Asp	Thr
	740	745	750	750												
	Val	Ser	Ala	Tyr	Ile	Pro	Asp	Ala	Ile	Trp	Tyr	Asp	Tyr	Glu	Ser	Gly
10	755	760	765	765												
	Ala	Lys	Arg	Pro	Trp	Arg	Lys	Gln	Arg	Val	Asp	Met	Tyr	Leu	Pro	Ala
	770	775	780	780												
	Asp	Lys	Ile	Gly	Leu	His	Leu	Arg	Gly	Gly	Tyr	Ile	Ile	Pro	Ile	Gln
	785	790	795	800												
	Glu	Pro	Asp	Val	Thr	Thr	Ala	Ser	Arg	Lys	Asn	Pro	Leu	Gly	Leu	
	805	810	815	815												
	Ile	Val	Ala	Leu	Gly	Glu	Asn	Asn	Thr	Ala	Lys	Gly	Asp	Phe	Phe	Trp
	820	825	830	830												
	Asp	Asp	Gly	Glu	Thr	Lys	Asp	Thr	Ile	Gln	Asn	Gly	Asn	Tyr	Ile	Leu
15	835	840	845	845												
	Tyr	Thr	Phe	Ser	Val	Ser	Asn	Asn	Thr	Leu	Asp	Ile	Val	Cys	Thr	His
	850	855	860	860												
	Ser	Ser	Tyr	Gln	Glu	Gly	Thr	Thr	Leu	Ala	Phe	Gln	Thr	Val	Lys	Ile
	865	870	875	880												
	Leu	Gly	Leu	Thr	Asp	Ser	Val	Thr	Glu	Val	Arg	Val	Ala	Glu	Asn	Asn
	885	890	895	895												
	Gln	Pro	Met	Asn	Ala	His	Ser	Asn	Phe	Thr	Tyr	Asp	Ala	Ser	Asn	Gln
	900	905	910	910												
	Val	Leu	Leu	Ile	Ala	Asp	Leu	Lys	Leu	Asn	Leu	Gly	Arg	Asn	Phe	Ser
20	915	920	925	925												
	Val	Gln	Trp	Asn	Gln	Ile	Phe	Ser	Glu	Asn	Glu	Arg	Phe	Asn	Cys	Tyr
	930	935	940	940												
	Pro	Asp	Ala	Asp	Leu	Ala	Thr	Glu	Gln	Lys	Cys	Thr	Gln	Arg	Gly	Cys
	945	950	955	960												
	Val	Trp	Arg	Thr	Gly	Ser	Ser	Leu	Ser	Lys	Ala	Pro	Glu	Cys	Tyr	Phe
	965	970	975	975												
	Pro	Arg	Gln	Asp	Asn	Ser	Tyr	Ser	Val	Asn	Ser	Ala	Arg	Tyr	Ser	Ser
	980	985	990	990												
	Met	Gly	Ile	Thr	Ala	Asp	Leu	Gln	Leu	Asn	Thr	Ala	Asn	Ala	Arg	Ile
25	995	1000	1005	1005												
	Lys	Leu	Pro	Ser	Asp	Pro	Ile	Ser	Thr	Leu	Arg	Val	Glu	Val	Lys	Tyr
	1010	1015	1020	1020												
	His	Lys	Asn	Asp	Met	Leu	Gln	Phe	Lys	Ile	Tyr	Asp	Pro	Gln	Lys	Lys
	1025	1030	1035	1040												
	Arg	Tyr	Glu	Val	Pro	Val	Pro	Leu	Asn	Ile	Pro	Thr	Thr	Pro	Ile	Ser
	1045	1050	1055	1055												
	Thr	Tyr	Glu	Asp	Arg	Leu	Tyr	Asp	Val	Glu	Ile	Lys	Glu	Asn	Pro	Phe
	1060	1065	1070	1070												
	Gly	Ile	Gln	Ile	Arg	Arg	Arg	Ser	Ser	Gly	Arg	Val	Ile	Trp	Asp	Ser
	1075	1080	1085	1085												
30	1090	1095	1100	1100												

Arg Leu Pro Ser Glu Tyr Ile Tyr Gly Phe Gly Glu Val Glu His Thr
 105 1110 1115 1120
 Ala Phe Lys Arg Asp Leu Asn Trp Asn Thr Trp Gly Met Phe Thr Arg
 1125 1130 1135
 Asp Gln Pro Pro Gly Tyr Lys Leu Asn Ser Tyr Gly Phe His Pro Tyr
 1140 1145 1150
 Tyr Met Ala Leu Glu Glu Gly Asn Ala His Gly Val Phe Leu Leu
 1155 1160 1165
 5 Asn Ser Asn Ala Met Asp Val Thr Phe Gln Pro Thr Pro Ala Leu Thr
 1170 1175 1180
 Tyr Arg Thr Val Gly Gly Ile Leu Asp Phe Tyr Met Phe Leu Gly Pro
 185 1190 1195 1200
 Thr Pro Gln Val Ala Thr Lys Gln Tyr His Glu Val Ile Gly His Pro
 1205 1210 1215
 Val Met Pro Ala Tyr Trp Ala Leu Gly Phe Gln Leu Cys Arg Tyr Gly
 1220 1225 1230
 Tyr Ala Asn Thr Ser Glu Val Arg Glu Leu Tyr Asp Ala Met Val Ala
 1235 1240 1245
 10 Ala Asn Ile Pro Tyr Asp Val Gln Tyr Thr Asp Ile Asp Tyr Met Glu
 1250 1255 1260
 Arg Gln Leu Asp Phe Thr Ile Gly Glu Ala Phe Gln Asp Leu Pro Gln
 265 1270 1275 1280
 Phe Val Asp Lys Ile Arg Gly Glu Gly Met Arg Tyr Ile Ile Leu
 1285 1290 1295
 Asp Pro Ala Ile Ser Gly Asn Glu Thr Lys Thr Tyr Pro Ala Phe Glu
 1300 1305 1310
 Arg Gly Gln Gln Asn Asp Val Phe Val Lys Trp Pro Asn Thr Asn Asp
 1315 1320 1325
 15 Ile Cys Trp Ala Lys Val Trp Pro Asp Leu Pro Asn Ile Thr Ile Asp
 1330 1335 1340
 Lys Thr Leu Thr Glu Asp Glu Ala Val Asn Ala Ser Arg Ala His Val
 345 1350 1355 1360
 Ala Phe Pro Asp Phe Arg Thr Ser Thr Ala Glu Trp Trp Ala Arg
 1365 1370 1375
 Glu Ile Val Asp Phe Tyr Asn Glu Lys Met Lys Phe Asp Gly Leu Trp
 1380 1385 1390
 Ile Asp Met Asn Glu Pro Ser Ser Phe Val Asn Gly Thr Thr Asn
 1395 1400 1405
 20 Gln Cys Arg Asn Asp Glu Leu Asn Tyr Pro Pro Tyr Phe Pro Glu Leu
 1410 1415 1420
 Thr Lys Arg Thr Asp Gly Leu His Phe Arg Thr Ile Cys Met Glu Ala
 425 1430 1435 1440
 Glu Gln Ile Leu Ser Asp Gly Thr Ser Val Leu His Tyr Asp Val His
 1445 1450 1455
 Asn Leu Tyr Gly Trp Ser Gln Met Lys Pro Thr His Asp Ala Leu Gln
 1460 1465 1470
 Lys Thr Thr Gly Lys Arg Gly Ile Val Ile Ser Arg Ser Thr Tyr Pro
 1475 1480 1485
 25 Thr Ser Gly Arg Trp Gly Gly His Trp Leu Gly Asp Asn Tyr Ala Arg
 1490 1495 1500
 Trp Asp Asn Met Asp Lys Ser Ile Ile Gly Met Met Glu Phe Ser Leu
 505 1510 1515 1520
 Phe Gly Ile Ser Tyr Thr Gly Ala Asp Ile Cys Gly Phe Phe Asn Asn
 1525 1530 1535
 Ser Glu Tyr His Leu Cys Thr Arg Trp Met Gln Leu Gly Ala Phe Tyr
 1540 1545 1550
 Pro Tyr Ser Arg Asn His Asn Ile Ala Asn Thr Arg Arg Gln Asp Pro
 1555 1560 1565
 30 Ala Ser Trp Asn Glu Thr Phe Ala Glu Met Ser Arg Asn Ile Leu Asn
 1570 1575 1580
 Ile Arg Tyr Thr Leu Leu Pro Tyr Phe Tyr Thr Gln Met His Glu Ile

	585	1590	1595	1600
	His Ala Asn Gly Gly Thr Val Ile Arg Pro Leu Leu His Glu Phe Phe			
	1605	1610	1615	
	Asp Glu Lys Pro Thr Trp Asp Ile Phe Lys Gln Phe Leu Trp Gly Pro			
	1620	1625	1630	
	Ala Phe Met Val Thr Pro Val Leu Glu Pro Tyr Val Gln Thr Val Asn			
	1635	1640	1645	
5	Ala Tyr Val Pro Asn Ala Arg Trp Phe Asp Tyr His Thr Gly Lys Asp			
	1650	1655	1660	
	Ile Gly Val Arg Gly Gln Phe Gln Thr Phe Asn Ala Ser Tyr Asp Thr			
	665	1670	1675	1680
	Ile Asn Leu His Val Arg Gly Gly His Ile Leu Pro Cys Gln Glu Pro			
	1685	1690	1695	
	Ala Gln Asn Thr Phe Tyr Ser Arg Gln Lys His Met Lys Leu Ile Val			
	1700	1705	1710	
	Ala Ala Asp Asp Asn Gln Met Ala Gln Gly Ser Leu Phe Trp Asp Asp			
	1715	1720	1725	
10	Gly Glu Ser Ile Asp Thr Tyr Glu Arg Asp Leu Tyr Leu Ser Val Gln			
	1730	1735	1740	
	Phe Asn Leu Asn Gln Thr Thr Leu Thr Ser Thr Ile Leu Lys Arg Gly			
	745	1750	1755	1760
	Tyr Ile Asn Lys Ser Glu Thr Arg Leu Gly Ser Leu His Val Trp Gly			
	1765	1770	1775	
	Lys Gly Thr Thr Pro Val Asn Ala Val Thr Leu Thr Tyr Asn Gly Asn			
	1780	1785	1790	
	Lys Asn Ser Leu Pro Phe Asn Glu Asp Thr Thr Asn Met Ile Leu Arg			
	1795	1800	1805	
	Ile Asp Leu Thr Thr His Asn Val Thr Leu Glu Glu Pro Ile Glu Ile			
15	1810	1815	1820	
	Asn Trp Ser			
	825			

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2284 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 45...2099
 - (D) OTHER INFORMATION:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

25	GCCTTACTGC AGGAAGGCAC TCCGAAGACA TAAGTCGGTG AGAC ATG GCT GAA GAT	56
	Met Ala Glu Asp	
	1	
	AAA AGC AAG AGA GAC TCC ATC GAG ATG AGT ATG AAG GGA TGC CAG ACA	104
	Lys Ser Lys Arg Asp Ser Ile Glu Met Ser Met Lys Gly Cys Gln Thr	
	5 10 15 20	
30	AAC AAC GGG TTT GTC CAT AAT GAA GAC ATT CTG GAG CAG ACC CCG GAT	152
	Asn Asn Gly Phe Val His Asn Glu Asp Ile Leu Glu Gln Thr Pro Asp	
	25 30 35	

	CCA GGC AGC TCA ACA GAC AAC CTG AAG CAC AGC ACC AGG GGC ATC CTT	200
	Pro Gly Ser Ser Thr Asp Asn Leu Lys His Ser Thr Arg Gly Ile Leu	
	40 45 50	
	GGC TCC CAG GAG CCC GAC TTC AAG GGC GTC CAG CCC TAT GCG GGG ATG	248
	Gly Ser Gln Glu Pro Asp Phe Lys Gly Val Gln Pro Tyr Ala Gly Met	
	55 60 65	
5	CCC AAG GAG GTG CTG TTC CAG TTC TCT GGC CAG GCC CGC TAC CGC ATA	296
	Pro Lys Glu Val Leu Phe Gln Phe Ser Gly Gln Ala Arg Tyr Arg Ile	
	70 75 80	
	CCT CGG GAG ATC CTC TTC TGG CTC ACA GTG GCT TCT GTG CTG GTG CTC	344
	Pro Arg Glu Ile Leu Phe Trp Leu Thr Val Ala Ser Val Leu Val Leu	
	85 90 95 100	
	ATC GCG GCC ACC ATA GCC ATC ATT GCC CTC TCT CCA AAG TGC CTA GAC	392
	Ile Ala Ala Thr Ile Ala Ile Ile Ala Leu Ser Pro Lys Cys Leu Asp	
10	105 110 115	
	TGG TGG CAG GAG GGG CCC ATG TAC CAG ATC TAC CCA AGG TCT TTC AAG	440
	Trp Trp Gln Glu Gly Pro Met Tyr Gln Ile Tyr Pro Arg Ser Phe Lys	
	120 125 130	
	GAC AGT AAC AAG GAT GGG AAC GGA GAT CTG AAA GGT ATT CAA GAT AAA	488
	Asp Ser Asn Lys Asp Gly Asn Gly Asp Leu Lys Gly Ile Gln Asp Lys	
	135 140 145	
15	CTG GAC TAC ATC ACA GCT TTA AAT ATA AAA ACT GTT TGG ATT ACT TCA	536
	Leu Asp Tyr Ile Thr Ala Leu Asn Ile Lys Thr Val Trp Ile Thr Ser	
	150 155 160	
	TTT TAT AAA TCG TCC CTT AAA GAT TTC AGA TAT GGT GTT GAA GAT TTC	584
	Phe Tyr Lys Ser Ser Leu Lys Asp Phe Arg Tyr Gly Val Glu Asp Phe	
	165 170 175 180	
	CGG GAA GTT GAT CCC ATT TTT GGA ACG ATG GAA GAT TTT GAG AAT CTG	632
	Arg Glu Val Asp Pro Ile Phe Gly Thr Met Glu Asp Phe Glu Asn Leu	
20	185 190 195	
	GTT GCA GCC ATA CAT GAT AAA GGT TTA AAA TTA ATC ATC GAT TTC ATA	680
	Val Ala Ala Ile His Asp Lys Gly Leu Lys Leu Ile Ile Asp Phe Ile	
	200 205 210	
	CCA AAC CAC ACG AGT GAT AAA CAT ATT TGG TTT CAA TTG AGT CGG ACA	728
	Pro Asn His Thr Ser Asp Lys His Ile Trp Phe Gln Leu Ser Arg Thr	
	215 220 225	
25	CGG ACA GGA AAA TAT ACT GAT TAT TAT ATC TGG CAT GAC TGT ACC CAT	776
	Arg Thr Gly Lys Tyr Thr Asp Tyr Tyr Ile Trp His Asp Cys Thr His	
	230 235 240	
	GAA AAT GGC AAA ACC ATT CCA CCC AAC AAC TGG TTA AGT GTG TAT GGA	824
	Glu Asn Gly Lys Thr Ile Pro Pro Asn Asn Trp Leu Ser Val Tyr Gly	
	245 250 255 260	
	AAC TCC AGT TGG CAC TTT GAC GAA GTG CGA AAC CAA TGT TAT TTT CAT	872
	Asn Ser Ser Trp His Phe Asp Glu Val Arg Asn Gln Cys Tyr Phe His	
30	265 270 275	
	CAG TTT ATG AAA GAG CAA CCT GAT TTA AAT TTC CGC AAT CCT GAT GTT	920

	Gln Phe Met Lys Glu Gln Pro Asp Leu Asn Phe Arg Asn Pro Asp Val			
	280	285	290	
	CAA GAA GAA ATA AAA GAA ATT TTA CGG TTC TGG CTC ACA AAG GGT GTT		968	
	Gln Glu Ile Lys Glu Ile Leu Arg Phe Trp Leu Thr Lys Gly Val			
	295	300	305	
5	GAT GGT TTT AGT TTG GAT GCT GTT AAA TTC CTC CTA GAA GCA AAG CAC		1016	
	Asp Gly Phe Ser Leu Asp Ala Val Lys Phe Leu Leu Glu Ala Lys His			
	310	315	320	
	CTG AGA GAT GAG ATC CAA GTA AAT AAG ACC CAA ATC CCG GAC ACG GTC		1064	
	Leu Arg Asp Glu Ile Gln Val Asn Lys Thr Gln Ile Pro Asp Thr Val			
	325	330	335	340
	ACA CAA TAC TCG GAG CTG TAC CAT GAC TTC ACC ACC ACG CAG GTG GGA		1112	
	Thr Gln Tyr Ser Glu Leu Tyr His Asp Phe Thr Thr Thr Gln Val Gly			
	345	350	355	
10	ATG CAC GAC ATT GTC CGC AGC TTC CGG CAG ACC ATG GAC CAA TAC AGC		1160	
	Met His Asp Ile Val Arg Ser Phe Arg Gln Thr Met Asp Gln Tyr Ser			
	360	365	370	
	ACG GAG CCC GGC AGA TAC AGG TTC ATG GGG ACT GAA GCC TAT GCA GAG		1208	
	Thr Glu Pro Gly Arg Tyr Arg Phe Met Gly Thr Glu Ala Tyr Ala Glu			
	375	380	385	
15	AGT ATT GAC AGG ACC GTG ATG TAC TAT GGA TTG CCA TTT ATC CAA GAA		1256	
	Ser Ile Asp Arg Thr Val Met Tyr Tyr Gly Leu Pro Phe Ile Gln Glu			
	390	395	400	
	GCT GAT TTT CCC TTC AAC AAT TAC CTC AGC ATG CTA GAC ACT GTT TCT		1304	
	Ala Asp Phe Pro Phe Asn Asn Tyr Leu Ser Met Leu Asp Thr Val Ser			
	405	410	415	420
	GGG AAC AGC GTG TAT GAG GTT ATC ACA TCC TGG ATG GAA AAC ATG CCA		1352	
	Gly Asn Ser Val Tyr Glu Val Ile Thr Ser Trp Met Glu Asn Met Pro			
	425	430	435	
20	GAA GGA AAA TGG CCT AAC TGG ATG ATT GGT GGA CCA GAC AGT TCA CGG		1400	
	Glu Gly Lys Trp Pro Asn Trp Met Ile Gly Gly Pro Asp Ser Ser Arg			
	440	445	450	
	CTG ACT TCG CGT TTG GGG AAT CAG TAT GTC AAC GTG ATG AAC ATG CTT		1448	
	Leu Thr Ser Arg Leu Gly Asn Gln Tyr Val Asn Val Met Asn Met Leu			
	455	460	465	
25	CTT TTC ACA CTC CCT GGA ACT CCT ATA ACT TAC TAT GGA GAA GAA ATT		1496	
	Leu Phe Thr Leu Pro Gly Thr Pro Ile Thr Tyr Tyr Gly Glu Glu Ile			
	470	475	480	
	GGA ATG GGA AAT ATT GTA GCC GCA AAT CTC AAT GAA AGC TAT GAT ATT		1544	
	Gly Met Gly Asn Ile Val Ala Ala Asn Leu Asn Glu Ser Tyr Asp Ile			
	485	490	495	500
	AAT ACC CTT CGC TCA AAG TCA CCA ATG CAG TGG GAC AAT AGT TCA AAT		1592	
	Asn Thr Leu Arg Ser Lys Ser Pro Met Gln Trp Asp Asn Ser Ser Asn			
	505	510	515	
30	GCT GGT TTT TCT GAA GCT AGT AAC ACC TGG TTA CCT ACC AAT TCA GAT		1640	
	Ala Gly Phe Ser Glu Ala Ser Asn Thr Trp Leu Pro Thr Asn Ser Asp			

	520	525	530	
	TAC CAC ACT GTG AAT GTT GAT GTC CAA AAG ACT CAG CCC AGA TCG GCT			1688
	Tyr His Thr Val Asn Val Asp Val Gln Lys Thr Gln Pro Arg Ser Ala			
	535	540	545	
5	TTG AAG TTA TAT CAA GAT TTA AGT CTA CTT CAT GCC AAT GAG CTA CTC			1736
	Leu Lys Leu Tyr Gln Asp Leu Ser Leu Leu His Ala Asn Glu Leu Leu			
	550	555	560	
	CTC AAC AGG GGC TGG TTT TGC CAT TTG AGG AAT GAC AGC CAC TAT GTT			1784
	Leu Asn Arg Gly Trp Phe Cys His Leu Arg Asn Asp Ser His Tyr Val			
	565	570	575	580
	GTG TAC ACA AGA GAG CTG GAT GGC ATC GAC AGA ATC TTT ATC GTG GTT			1832
	Val Tyr Thr Arg Glu Leu Asp Gly Ile Asp Arg Ile Phe Ile Val Val			
	585	590	595	
10	CTG AAT TTT GGA GAA TCA ACA CTG TTA AAT CTA CAT AAT ATG ATT TCG			1880
	Leu Asn Phe Gly Glu Ser Thr Leu Leu Asn Leu His Asn Met Ile Ser			
	600	605	610	
	GGC CTT CCC GCT AAA ATA AGA ATA AGG TTA AGT ACC AAT TCT GCC GAC			1928
	Gly Leu Pro Ala Lys Ile Arg Ile Arg Leu Ser Thr Asn Ser Ala Asp			
	615	620	625	
15	AAA GGC AGT AAA GTT GAT ACA AGT GGC ATT TTT CTG GAC AAG GGA GAG			1976
	Lys Gly Ser Lys Val Asp Thr Ser Gly Ile Phe Leu Asp Lys Gly Glu			
	630	635	640	
	GGA CTC ATC TTT GAA CAC AAC ACG AAG AAT CTC CTT CAT CGC CAA ACA			2024
	Gly Leu Ile Phe Glu His Asn Thr Lys Asn Leu Leu His Arg Gln Thr			
	645	650	655	660
	GCT TTC AGA GAT AGA TGC TTT GTT TCC AAT CGA GCA TGC TAT TCC AGT			2072
	Ala Phe Arg Asp Arg Cys Phe Val Ser Asn Arg Ala Cys Tyr Ser Ser			
	665	670	675	
20	GTA CTG AAC ATA CTG TAT ACC TCG TGT TAGGCACCTT TATGAAGAGA TGAAGAC			2126
	Val Leu Asn Ile Leu Tyr Thr Ser Cys			
	680	685		
	ACTGGCATTT CAGTGGGATT GTAAGCATT GTAAATAGCTT CATGTACAGC ATGCTGCTTG			2186
	GTGAACAATC ATTAATTCTT CGATATTCT GTAGCTTGAA TGTAACCGCT TTAAGAAAGG			2246
	TTCTCAAATG TTTGAAAAA AATAAAATGT TTAAAAGT			2284

(2) INFORMATION FOR SEQ ID NO:181:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 685 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:
- 30 Met Ala Glu Asp Lys Ser Lys Arg Asp Ser Ile Glu Met Ser Met Lys
 1 5 10 15
 Gly Cys Gln Thr Asn Asn Gly Phe Val His Asn Glu Asp Ile Leu Glu

	20	25	30													
Gln	Thr	Pro	Asp	Pro	Gly	Ser	Ser	Thr	Asp	Asn	Leu	Lys	His	Ser	Thr	
35							40					45				
Arg	Gly	Ile	Leu	Gly	Ser	Gln	Glu	Pro	Asp	Phe	Lys	Gly	Val	Gln	Pro	
50							55					60				
Tyr	Ala	Gly	Met	Pro	Lys	Glu	Val	Leu	Phe	Gln	Phe	Ser	Gly	Gln	Ala	
65							70					75			80	
Arg	Tyr	Arg	Ile	Pro	Arg	Glu	Ile	Leu	Phe	Trp	Leu	Thr	Val	Ala	Ser	
							85					90			95	
5	Val	Leu	Val	Leu	Ile	Ala	Ala	Thr	Ile	Ala	Ile	Ile	Ala	Leu	Ser	Pro
							100					105			110	
Lys	Cys	Leu	Asp	Trp	Trp	Gln	Glu	Gly	Pro	Met	Tyr	Gln	Ile	Tyr	Pro	
							115					120			125	
Arg	Ser	Phe	Lys	Asp	Ser	Asn	Lys	Asp	Gly	Asn	Gly	Asp	Leu	Lys	Gly	
							130					135			140	
Ile	Gln	Asp	Lys	Leu	Asp	Tyr	Ile	Thr	Ala	Leu	Asn	Ile	Lys	Thr	Val	
145							150					155			160	
Trp	Ile	Thr	Ser	Phe	Tyr	Lys	Ser	Ser	Leu	Lys	Asp	Phe	Arg	Tyr	Gly	
							165					170			175	
10	Val	Glu	Asp	Phe	Arg	Glu	Val	Asp	Pro	Ile	Phe	Gly	Thr	Met	Glu	Asp
							180					185			190	
Phe	Glu	Asn	Leu	Val	Ala	Ala	Ile	His	Asp	Lys	Gly	Leu	Lys	Leu	Ile	
							195					200			205	
Ile	Asp	Phe	Ile	Pro	Asn	His	Thr	Ser	Asp	Lys	His	Ile	Trp	Phe	Gln	
							210					215			220	
Leu	Ser	Arg	Thr	Arg	Thr	Gly	Lys	Tyr	Thr	Asp	Tyr	Tyr	Ile	Trp	His	
225							230					235			240	
Asp	Cys	Thr	His	Glu	Asn	Gly	Lys	Thr	Ile	Pro	Pro	Asn	Asn	Trp	Leu	
							245					250			255	
15	Ser	Val	Tyr	Gly	Asn	Ser	Ser	Trp	His	Phe	Asp	Glu	Val	Arg	Asn	Gln
							260					265			270	
Cys	Tyr	Phe	His	Gln	Phe	Met	Lys	Glu	Gln	Pro	Asp	Leu	Asn	Phe	Arg	
							275					280			285	
Asn	Pro	Asp	Val	Gln	Glu	Glu	Ile	Lys	Glu	Ile	Leu	Arg	Phe	Trp	Leu	
							290					295			300	
Thr	Lys	Gly	Val	Asp	Gly	Phe	Ser	Leu	Asp	Ala	Val	Lys	Phe	Leu	Leu	
305							310					315			320	
Glu	Ala	Lys	His	Leu	Arg	Asp	Glu	Ile	Gln	Val	Asn	Lys	Thr	Gln	Ile	
							325					330			335	
20	Pro	Asp	Thr	Val	Thr	Gln	Tyr	Ser	Glu	Leu	Tyr	His	Asp	Phe	Thr	Thr
							340					345			350	
Thr	Gln	Val	Gly	Met	His	Asp	Ile	Val	Arg	Ser	Phe	Arg	Gln	Thr	Met	
							355					360			365	
Asp	Gln	Tyr	Ser	Thr	Glu	Pro	Gly	Arg	Tyr	Arg	Phe	Met	Gly	Thr	Glu	
							370					375			380	
Ala	Tyr	Ala	Glu	Ser	Ile	Asp	Arg	Thr	Val	Met	Tyr	Tyr	Gly	Leu	Pro	
385							390					395			400	
Phe	Ile	Gln	Glu	Ala	Asp	Phe	Pro	Phe	Asn	Asn	Tyr	Leu	Ser	Met	Leu	
							405					410			415	
25	Asp	Thr	Val	Ser	Gly	Asn	Ser	Val	Tyr	Glu	Val	Ile	Thr	Ser	Trp	Met
							420					425			430	
Glu	Asn	Met	Pro	Glu	Gly	Lys	Trp	Pro	Asn	Trp	Met	Ile	Gly	Gly	Pro	
							435					440			445	
Asp	Ser	Ser	Arg	Leu	Thr	Ser	Arg	Leu	Gly	Asn	Gln	Tyr	Val	Asn	Val	
							450					455			460	
Met	Asn	Met	Leu	Leu	Phe	Thr	Leu	Pro	Gly	Thr	Pro	Ile	Thr	Tyr	Tyr	
465							470					475			480	
Gly	Glu	Glu	Ile	Gly	Met	Gly	Asn	Ile	Val	Ala	Ala	Asn	Leu	Asn	Glu	
							485					490			495	
30	Ser	Tyr	Asp	Ile	Asn	Thr	Leu	Arg	Ser	Lys	Ser	Pro	Met	Gln	Trp	Asp
							500					505			510	

	Asn	Ser	Ser	Asn	Ala	Gly	Phe	Ser	Glu	Ala	Ser	Asn	Thr	Trp	Leu	Pro
	515						520							525		
	Thr	Asn	Ser	Asp	Tyr	His	Thr	Val	Asn	Val	Asp	Val	Gln	Lys	Thr	Gln
	530						535							540		
	Pro	Arg	Ser	Ala	Leu	Lys	Leu	Tyr	Gln	Asp	Leu	Ser	Leu	Leu	His	Ala
	545						550							555		560
	Asn	Glu	Leu	Leu	Leu	Asn	Arg	Gly	Trp	Phe	Cys	His	Leu	Arg	Asn	Asp
							565			570				575		
5	Ser	His	Tyr	Val	Val	Tyr	Thr	Arg	Glu	Leu	Asp	Gly	Ile	Asp	Arg	Ile
							580			585				590		
	Phe	Ile	Val	Val	Leu	Asn	Phe	Gly	Glu	Ser	Thr	Leu	Leu	Asn	Leu	His
							595			600				605		
	Asn	Met	Ile	Ser	Gly	Leu	Pro	Ala	Lys	Ile	Arg	Ile	Arg	Leu	Ser	Thr
	610						615							620		
	Asn	Ser	Ala	Asp	Lys	Gly	Ser	Lys	Val	Asp	Thr	Ser	Gly	Ile	Phe	Leu
	625						630							635		640
	Asp	Lys	Gly	Glu	Gly	Leu	Ile	Phe	Glu	His	Asn	Thr	Lys	Asn	Leu	Leu
							645			650				655		
10	His	Arg	Gln	Thr	Ala	Phe	Arg	Asp	Arg	Cys	Phe	Val	Ser	Asn	Arg	Ala
							660			665				670		
	Cys	Tyr	Ser	Ser	Val	Leu	Asn	Ile	Leu	Tyr	Thr	Ser	Cys			
							675			680				685		

(2) INFORMATION FOR SEQ ID NO:182:

	(i)	SEQUENCE CHARACTERISTICS:														
	(A)	LENGTH: 54 amino acids														
	(B)	TYPE: amino acid														
15	(C)	STRANDEDNESS:														
	(D)	TOPOLOGY: unknown														
	(ii)	MOLECULE TYPE: peptide														
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:182:														
	Leu	Val	Pro	Arg	Gly	Ser	Pro	Gly	Ile	Pro	Gly	Ser	Arg	Val	Gly	Gln
	1				5				10						15	
	Cys	Thr	Asp	Ser	Asp	Val	Arg	Arg	Pro	Trp	Ala	Arg	Ser	Cys	Ala	His
20							20			25					30	
	Gln	Gly	Cys	Gly	Ala	Gly	Thr	Arg	Asn	Ser	His	Gly	Cys	Ile	Thr	Arg
							35			40				45		
	Pro	Leu	Arg	Gln	Ala	Ser										
						50										

(2) INFORMATION FOR SEQ ID NO:183:

	(i)	SEQUENCE CHARACTERISTICS:														
	(A)	LENGTH: 19 amino acids														
25	(B)	TYPE: amino acid														
	(C)	STRANDEDNESS:														
	(D)	TOPOLOGY: unknown														
	(ii)	MOLECULE TYPE: peptide														
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:183:														
	Ser	Ala	Arg	Asp	Ser	Gly	Pro	Ala	Glu	Asp	Gly	Ser	Arg	Ala	Val	Arg
	1				5				10						15	
	Leu	Asn	Gly													
30																

(2) INFORMATION FOR SEQ ID NO:184:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

5 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Asp Gly Ser Arg Ala Val Arg Leu Asn Gly Val Glu Asn Ala Asn Thr
1 5 10 15
Arg Lys Ser Ser Arg
20

(2) INFORMATION FOR SEQ ID NO:185:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

15 Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly Arg
1 5 10 15
Arg His Pro

(2) INFORMATION FOR SEQ ID NO:186:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly
1 5 10

25 (2) INFORMATION FOR SEQ ID NO:187:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Ser Arg Pro Tyr Ser Val Asp Ser Asp Ser Asp Thr Asn Ala Lys His
1 5 10 15
Ser Ser His Asn Arg
20

(2) INFORMATION FOR SEQ ID NO:188:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

10 Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg Ser
1 5 10 15
Arg Pro Asn

(2) INFORMATION FOR SEQ ID NO:189:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

Arg Tyr Lys His Asp Ile Gly Cys Asp Ala Gly Val Asp Lys Lys Ser
1 5 10 15
Ser Ser Val Arg Gly Gly Cys Gly
20

20 (2) INFORMATION FOR SEQ ID NO:190:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Gly Cys Asp Ala Gly Val Asp Lys Lys Ser Ser Ser Val Arg Gly Gly
1 5 10 15
Cys Gly Ala His Ser Ser Pro Pro Arg Ala
20 25

(2) INFORMATION FOR SEQ ID NO:191:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

5 Gly Ala His Ser Ser Pro Pro Arg Ala Gly Arg Gly Pro Arg Gly Thr
1 5 10 15
Met Val Ser Arg Leu
20

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
10 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:193:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

20 Lys Lys Arg Ile Ala Gly Leu Pro Trp Tyr Arg Cys Arg Thr Val Ala
1 5 10 15
Phe Glu Thr Gly Met Gln Asn Thr Gln Leu Cys Ser Thr Ile Val Gln
20 25 30
Leu Ser Phe Thr Pro Glu Glu
35

(2) INFORMATION FOR SEQ ID NO:194:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

30 Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

5 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

Ser Asn Pro Arg Gly Arg Arg His Pro
1 5

(2) INFORMATION FOR SEQ ID NO:196:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

15 Thr Asn Ala Lys His Ser Ser His Asn
1 5

(2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

20 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

Ser Ser His Asn Arg Arg Leu Arg Thr Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:198:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Arg Arg Leu Arg Thr Arg Ser Arg Pro Asn
1 5 10

30 (2) INFORMATION FOR SEQ ID NO:199:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

Arg Val Gly Gln Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala Arg
1 5 10 15
Ser Cys Ala

(2) INFORMATION FOR SEQ ID NO:200:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

15 Val Arg Arg Pro Trp Ala Arg Ser Cys Ala His Gln Gly Cys Gly Ala
1 5 10 15
Gly Thr Arg Asn Ser
20

(2) INFORMATION FOR SEQ ID NO:201:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

Gly Thr Arg Asn Ser His Gly Cys Ile Thr Arg Pro Leu Arg Gln Ala
1 5 10 15
Ser Gln His

25 (2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp
1 5 10 15
Ser Asp Ser Asp Thr Met Ala Lys His Ser Ser His Asn Arg Arg Leu
20 25 30
Arg Thr Arg Ser Arg Pro Asn Gly
35 40

(2) INFORMATION FOR SEQ ID NO:203:

5

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

10

Tyr Ser Lys Val
1

(2) INFORMATION FOR SEQ ID NO:204:

15

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Phe Pro His Leu
1

(2) INFORMATION FOR SEQ ID NO:205:

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

25

Tyr Arg Gly Val
1

(2) INFORMATION FOR SEQ ID NO:206:

30

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Tyr Gln Thr Ile
1

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

Thr Glu Gln Phe
10 1

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

15 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Thr Glu Val Met
1

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

Thr Ser Ala Phe
25 1

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

30 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Tyr Thr Arg Phe
1

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs
(B) TYPE: nucleic acid
5 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...714

(D) OTHER INFORMATION:

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

ATG	TCC	CCT	ATA	CTA	GGT	TAT	TGG	AAA	ATT	AAG	GGC	CTT	GTG	CAA	CCC	48	
Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro		
1				5					10					15			
ACT	CGA	CTT	CTT	TTG	GAA	TAT	CTT	GAA	GAA	AAA	TAT	GAA	GAG	CAT	TTG	96	
Thr	Arg	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	Glu	His	Leu		
20				25						30							
TAT	GAG	CGC	GAT	GAA	GGT	GAT	AAA	TGG	CGA	AAC	AAA	AAG	TTT	GAA	TTG	144	
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu		
35				40						45							
GGT	TTG	GAG	TTT	CCC	AAT	CTT	CCT	TAT	TAT	ATT	GAT	GGT	GAT	GTT	AAA	192	
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys		
50				55						60							
TTA	ACA	CAG	TCT	ATG	GCC	ATC	ATA	CGT	TAT	ATA	GCT	GAC	AAG	CAC	AAC	240	
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn		
20				65			70		75			80					
ATG	TTG	GGT	GGT	TGT	CCA	AAA	GAG	CGT	GCA	GAG	ATT	TCA	ATG	CTT	GAA	288	
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu		
85				90						95							
GGA	GCG	GTT	TTG	GAT	ATT	AGA	TAC	GGT	GTT	TCG	AGA	ATT	GCA	TAT	AGT	336	
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser		
100				105						110							
25	AAA	GAC	TTT	GAA	ACT	CTC	AAA	GTT	GAT	TTT	CTT	AGC	AAG	CTA	CCT	GAA	384
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu		
115				120						125							
ATG	CTG	AAA	ATG	TTC	GAA	GAT	CGT	TTA	TGT	CAT	AAA	ACA	TAT	TTA	AAT	432	
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn		
130				135						140							
GGT	GAT	CAT	GTA	ACC	CAT	CCT	GAC	TTC	ATG	TTG	TAT	GAC	GCT	CTT	GAT	480	
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp		
30	145			150						155			160				

	GTT	GTT	TTA	TAC	ATG	GAC	CCA	ATG	TGC	CTG	GAT	GCG	TTC	CCA	AAA	TTA	528
	Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu	
					165					170					175		
	GTT	TGT	TTT	AAA	AAA	CGT	ATT	GAA	GCT	ATC	CCA	CAA	ATT	GAT	AAG	TAC	576
	Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr	
					180					185					190		
5	TTG	AAA	TCC	AGC	AAG	TAT	ATA	GCA	TGG	CCT	TTG	CAG	GGC	TGG	CAA	GCC	624
	Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala	
					195					200					205		
	ACG	TTT	GGT	GGT	GGC	GAC	CAT	CCT	CCA	AAA	TCG	GAT	CTG	GTT	CCG	CGT	672
	Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg	
					210					215					220		
	GGA	TCC	CCA	GGA	ATT	CCC	GGG	TCG	ACT	CGA	GCG	GCC	GCA	TCG	TGA	717	
	Gly	Ser	Pro	Gly	Ile	Pro	Gly	Ser	Thr	Arg	Ala	Ala	Ala	Ser			
10					225					230					235		

(2) INFORMATION FOR SEQ ID NO:212:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 238 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

15 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

	Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro	
	1				5				10					15			
	Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu
								20		25				30			
	Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu	
								35		40				45			
20	Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys	
							50		55				60				
	Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn	
							65		70			75			80		
	Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu	
							85				90				95		
	Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser	
							100			105				110			
	Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	
							115			120				125			
25	Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	
							130			135				140			
	Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	
							145			150			155			160	
	Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu	
							165			170					175		
	Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr	
							180			185					190		
	Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala	
							195			200					205		
30	Thr	Phe	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg		
							210			215					220		

Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser
225 230 235

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

5

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1 5 10 15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
10 20 25 30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35 40 45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65 70 75 80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85 90 95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100 105 110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115 120 125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130 135 140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145 150 155 160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165 170 175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180 185 190
20 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195 200 205
Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
210 215 220
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Gln
225 230 235 240
Gly Ser Lys Gln Cys Met Gln Tyr Arg Thr Gly Arg Leu Thr Val Gly
245 250 255
Ser Glu Tyr Gly Cys Gly Met Asn Pro Ala Arg His Ala Thr Pro Ala
260 265 270
25 Tyr Pro Ala Arg Leu Leu Pro Arg Tyr Arg
275 280

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

30

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1 5 10 15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20 25 30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35 40 45
5 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65 70 75 80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85 90 95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100 105 110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115 120 125
10 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130 135 140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145 150 155 160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165 170 175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180 185 190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195 200 205
15 Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
210 215 220
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Asp
225 230 235 240
His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys Glu Pro Gly
245 250 255
Asp Tyr Asn Cys Cys Gly Asn Ser Thr Gly Arg Lys Val Phe
260 265 270
Asn Arg Arg Arg Pro Ser Ala Ile Pro Thr
275 280

20 (2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 279 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1 5 10 15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20 25 30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35 40 45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60
30 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65 70 75 80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
5 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
10 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Pro
 225 230 235 240
 Cys Gly Gly Ser Trp Gly Arg Phe Met Gln Gly Gly Leu Phe Gly Gly
 245 250 255
 Arg Thr Asp Gly Cys Gly Ala His Arg Asn Arg Thr Ser Ala Ser Leu
 260 265 270
 Glu Pro Pro Ser Ser Asp Tyr
 275

(2) INFORMATION FOR SEQ ID NO:216:

15

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 277 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

20

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80

25

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160

30

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Arg Gly
 225 230 235 240
5 Ser Thr Gly Thr Ala Gly Gly Glu Arg Ser Gly Val Leu Asn Leu His
 245 250 255
 Thr Arg Asp Asn Ala Ser Gly Ser Gly Phe Lys Pro Trp Tyr Pro Ser
 260 265 270
 Asn Arg Gly His Lys
 275

(2) INFORMATION FOR SEQ ID NO:217:

- 10** (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 277 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
15 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
20 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
25 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser His
 225 230 235 240
 Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val Phe Arg Glu Leu Arg
 245 250 255
30 Asp Arg Trp Asn Ala Thr Ser His His Thr Arg Pro Thr Pro Gln Leu
 260 265 270

Pro Arg Gly Pro Asn
275

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
(B) TYPE: amino acid
5 (C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1 5 10 15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
10 20 25 30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35 40 45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65 70 75 80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85 90 95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
15 100 105 110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115 120 125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130 135 140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145 150 155 160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165 170 175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
20 180 185 190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195 200 205
Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
210 215 220
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser His
225 230 235 240
Ser Gly Gly Met Asn Arg Ala Tyr
245

25 (2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro

	1	5	10	15
	Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu			
	20	25	30	
	Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu			
	35	40	45	
	Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys			
	50	55	60	
	Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn			
5	65	70	75	80
	Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu			
	85	90	95	
	Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser			
	100	105	110	
	Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu			
	115	120	125	
	Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn			
	130	135	140	
	Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp			
10	145	150	155	160
	Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu			
	165	170	175	
	Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr			
	180	185	190	
	Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala			
	195	200	205	
	Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg			
	210	215	220	
	Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Gly Asp			
15	225	230	235	240
	Val Phe Arg Glu Leu Arg Asp Arg			
	245			

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

20 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

	1	5	10	15
	Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro			
	20	25	30	
	Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu			
	35	40	45	
	Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu			
	50	55	60	
	Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys			
	65	70	75	80
	Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn			
25	85	90	95	
	Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu			
	100	105	110	
	Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser			
30	115	120	125	
	Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu			
	Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn			

(2) INFORMATION FOR SEQ ID NO:221:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 247 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

 (ii) MOLECULE TYPE: peptide

 (xi) SEQUENCE DESCRIPTION: SEQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

15	Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro 1 5 10 15
	Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu 20 25 30
	Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu 35 40 45
	Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys 50 55 60
	Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn 65 70 75 80
20	Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu 85 90 95
	Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser 100 105 110
	Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu 115 120 125
	Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn 130 135 140
	Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp 145 150 155 160
25	Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu 165 170 175
	Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr 180 185 190
	Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala 195 200 205
	Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg 210 215 220
	Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Thr Pro 225 230 235 240
30	Gln Leu Pro Arg Gly Pro Asn 245

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 258 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

5 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1 5 10 15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20 25 30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35 40 45
10 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65 70 75 80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85 90 95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100 105 110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115 120 125
15 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130 135 140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145 150 155 160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165 170 175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180 185 190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195 200 205
20 Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
210 215 220
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Gly Asp
225 230 235 240
Val Phe Arg Glu Leu Arg Asp Arg Trp Asn Ala Thr Ser His His Thr
245 250 255
Arg Pro

(2) INFORMATION FOR SEQ ID NO:223:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 257 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

30 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1 5 10 15

Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
5 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
10 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Trp Asn
 225 230 235 240
15 Ala Thr Ser His His Thr Arg Pro Thr Pro Gln Leu Pro Arg Gly Pro
 245 250 255
 Asn

(2) INFORMATION FOR SEQ ID NO:224:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 267 amino acids
 (B) TYPE: amino acid
20 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
25 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
30 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
5 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Gly Asp
 225 230 235 240
 Val Phe Arg Glu Leu Arg Asp Arg Trp Asn Ala Thr Ser His His Thr
 245 250 255
 Arg Pro Thr Pro Gln Leu Pro Arg Gly Pro Asn
 260 265

10

(2) INFORMATION FOR SEQ ID NO:225:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 277 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
20 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
25 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
30 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ser Ser His
 225 230 235 240

Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val Phe Arg Glu Leu Arg
 245 250 255
 Asp Arg Trp Asn Ala Thr Ser Ala Ala Thr Arg Pro Thr Pro Gln Leu
 260 265 270
 Pro Arg Gly Pro Asn
 275

(2) INFORMATION FOR SEQ ID NO:226:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 277 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

10

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Ala
 225 230 235 240
 Arg Asp Ser Gly Pro Ala Glu Asp Gly Ser Arg Ala Val Arg Leu Asn
 245 250 255
 Gly Val Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg
 260 265 270
 Gly Arg Arg His Pro
 275

(2) INFORMATION FOR SEQ ID NO:227:

30

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 257 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

5	Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro			
	1	5	10	15
	Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu			
	20	25	30	
	Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu			
	35	40	45	
	Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys			
	50	55	60	
	Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn			
	65	70	75	80
10	Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu			
	85	90	95	
	Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser			
	100	105	110	
	Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu			
	115	120	125	
	Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn			
	130	135	140	
	Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp			
	145	150	155	160
15	Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu			
	165	170	175	
	Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr			
	180	185	190	
	Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala			
	195	200	205	
	Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg			
	210	215	220	
	Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Ala			
	225	230	235	240
20	Arg Asp Ser Gly Pro Ala Glu Asp Gly Ser Arg Ala Val Arg Leu Asn			
	245	250	255	
	Gly			

(2) INFORMATION FOR SEQ ID NO:228:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 259 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro			
1	5	10	15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu			
20	25	30	
30	Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu		
35	40	45	

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
5 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
10 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Asp Gly
 225 230 235 240
 Ser Arg Ala Val Arg Leu Asn Gly Val Glu Asn Ala Asn Thr Arg Lys
 245 250 255
 Ser Ser Arg

15 (2) INFORMATION FOR SEQ ID NO:229:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 257 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
25 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
30 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 5 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Glu Asn
 225 230 235 240
 Ala Asn Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly Arg Arg His
 245 250 255
 Pro

(2) INFORMATION FOR SEQ ID NO:230:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 248 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 15 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 20 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 25 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Glu Asn
 225 230 235 240
 Ala Asn Thr Arg Lys Ser Ser Arg
 245

30

(2) INFORMATION FOR SEQ ID NO:231:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 248 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1 5 10 15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20 25 30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35 40 45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60
10 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65 70 75 80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85 90 95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100 105 110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115 120 125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130 135 140
15 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145 150 155 160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165 170 175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180 185 190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195 200 205
Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
210 215 220
20 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Arg Lys
225 230 235 240
Ser Ser Arg Ser Asn Pro Arg Gly
245

(2) INFORMATION FOR SEQ ID NO:232:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 247 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1 5 10 15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20 25 30
30 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
5 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
10 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Asn
 225 230 235 240
 Pro Arg Gly Arg Arg His Pro
 245

(2) INFORMATION FOR SEQ ID NO:233:

15

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 249 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

20

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
25 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
30 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Thr Arg
 225 230 235 240
5 Lys Ser Ser Arg Ser Asn Pro Arg Gly
 245

(2) INFORMATION FOR SEQ ID NO:234:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 277 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

10

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
15 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
20 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
25 Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Thr
 225 230 235 240
 Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp Ser Asp
 245 250 255
 Ser Asp Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr
 260 265 270
 Arg Ser Arg Pro Asn
 275

30

(2) INFORMATION FOR SEQ ID NO:235:

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
- (A) NAME/KEY: Modified Site
(B) LOCATION: 1
(D) OTHER INFORMATION: "Xaa=Ser or Thr"
- (A) NAME/KEY: Modified Site
5 (B) LOCATION: 3
(D) OTHER INFORMATION: "Xaa=Arg or Lys"
- (A) NAME/KEY: Modified Site
(B) LOCATION: 4
(D) OTHER INFORMATION: "Xaa=Lys or Arg"
- (A) NAME/KEY: Modified Site
(B) LOCATION: 6
(D) OTHER INFORMATION: "Xaa=Ser or Leu"
- (A) NAME/KEY: Modified Site
10 (B) LOCATION: 7
(D) OTHER INFORMATION: "Xaa=Arg, Ile, Val or Ser"
- (A) NAME/KEY: Modified Site
(B) LOCATION: 8
(D) OTHER INFORMATION: "Xaa=Ser, Tyr, Phe or His"
- (A) NAME/KEY: Modified Site
15 (B) LOCATION: 10
(D) OTHER INFORMATION: "Xaa=Phe, His or Arg"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:
- Xaa Thr Xaa Xaa Ser Xaa Xaa Xaa Asn Xaa Arg
1 5 10
- (2) INFORMATION FOR SEQ ID NO:254:
- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
- (A) NAME/KEY: Modified Site
25 (B) LOCATION: 2
(D) OTHER INFORMATION: "Xaa=Ser, Ala or Gly"
- (A) NAME/KEY: Modified Site
(B) LOCATION: 4
(D) OTHER INFORMATION: "Xaa=Val or Gln"
- (A) NAME/KEY: Modified Site
(B) LOCATION: 7
(D) OTHER INFORMATION: "Xaa=Pro, Gly or Ser"
- 30 (A) NAME/KEY: Modified Site
(B) LOCATION: 8

(D) OTHER INFORMATION: "Xaa=Trp or Tyr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

Asp Xaa Asp Xaa Arg Arg Xaa Xaa
1 5

5 (2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

10 (A) NAME/KEY: Modified Site
(B) LOCATION: 7
(D) OTHER INFORMATION: "Xaa=Ala or Phe"

(A) NAME/KEY: Modified Site

(B) LOCATION: 8

(D) OTHER INFORMATION: "Xaa=Arg or His"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

15 Val Arg Ser Gly Cys Gly Xaa Xaa Ser Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

20 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

Asn Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:257:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

30 Ser Thr Lys Arg Ser Leu Ile Tyr Asn His Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:258:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

5 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

Ser Thr Gly Arg Lys Val Phe Asn Arg Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:259:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

15 Thr Asn Ala Lys His Ser Ser His Asn Arg Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:260:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

20 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

Asp Ser Asp Val Arg Arg Pro Trp
1 5

(2) INFORMATION FOR SEQ ID NO:261:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

Ala Ala Asp Gln Arg Arg Gly Trp
1 5

30 (2) INFORMATION FOR SEQ ID NO:262:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

Asp Gly Arg Gly Gly Arg Ser Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:263:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
10 (C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

Arg Val Arg Ser
1

15 (2) INFORMATION FOR SEQ ID NO:264:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

Ser Val Arg Ser Gly Cys Gly Phe Arg Gly Ser Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:265:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
25 (C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

Ser Val Arg Gly Gly Cys Gly Ala His Ser Ser
1 5 10

30 (2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- 5
 - (A) NAME/KEY: Other
 - (B) LOCATION: 2...2
 - (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

Cys Xaa Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly Arg Lys Lys
1 5 10 15
Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr His Gln Val
20 25 30
10 Ser Leu Ser Lys Gln
35

(2) INFORMATION FOR SEQ ID NO:267:

- 15
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 - (A) NAME/KEY: Other
 - (B) LOCATION: 1...1
 - (D) OTHER INFORMATION: Xaa=Ac-Cys

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

Xaa Leu Asn Gly Gly Val Lys Met Tyr Val Glu Ser Val Asp Arg Tyr
1 5 10 15
Val Cys

(2) INFORMATION FOR SEQ ID NO:268:

- 25
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 - (A) NAME/KEY: Other
 - (B) LOCATION: 1...1
 - (D) OTHER INFORMATION: Xaa=Ac-Cys

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

Xaa Leu Asn Gly Gly Val Lys Phe Ile Thr Cys Met Tyr Val Glu Ser
1 5 10 15
Val Asp Arg Tyr Val Cys
20

(2) INFORMATION FOR SEQ ID NO:269:

5

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

10

- (A) NAME/KEY: Other
(B) LOCATION: 2...2
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

Cys Xaa Arg Leu Asn Gly Gly Val Ser Met Tyr Val Glu Ser Val Asp
1 5 10 15
Arg Tyr Val Cys Arg
20

15

(2) INFORMATION FOR SEQ ID NO:270:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

20

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=biotin-Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

25 Xaa Ser Ala Arg Asp Ser Gly Pro Ala Glu Asp Gly Ser Arg Ala Val
1 5 10 15
Arg Leu Asn Gly Val Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg Ser
20 25 30
Asn Pro Arg Gly Arg Arg His Pro
35 40

(2) INFORMATION FOR SEQ ID NO:271:

30

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=biotin-Lys(dns)

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

Xaa Ser Ser Ala Asp Ala Glu Lys Cys Ala Gly Ser Leu Leu Trp Trp
1 5 10 15
Gly Arg Gln Asn Asn Ser Gly Cys Gly Ser Pro Thr Lys Lys His Leu
20 25 30
Lys His Arg Asn Arg Ser Gln Thr Ser Ser Ser His
35 40 45

10

(2) INFORMATION FOR SEQ ID NO:272:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=biotin-Lys(dns)

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

Xaa Arg Glu Phe Ala Glu Arg Arg Leu Trp Gly Cys Asp Asp Leu Ser
1 5 10 15
Trp Arg Leu Asp Ala Glu Gly Cys Gly Pro Thr Pro Ser Asn Arg Ala
20 25 30
Val Lys His Arg Lys Pro Arg Pro Arg Ser Pro Ala Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:273:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=biotin-Ser

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

Xaa Gly Ser His Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val Phe
1 5 10 15
Arg Glu Leu Arg Asp Arg Trp Tyr Ala Thr Ser His His Thr Arg Pro
20 25 30
Thr Pro Gln Leu Pro Arg Gly Pro Asn
35 40

(2) INFORMATION FOR SEQ ID NO:274:

5

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

10

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

Xaa Ser Gly Ser His Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val
1 5 10 15
Phe Arg Glu Leu Arg Asp Arg Trp Tyr Ala Thr Ser His His Thr Arg
20 25 30
15 Pro Thr Pro Gln Leu Pro Arg Gly Pro Asn
35 40

(2) INFORMATION FOR SEQ ID NO:275:

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=biotin-Lys(dns)

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

Xaa Ser His Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val Phe Arg
1 5 10 15
Glu Leu Arg Asp Arg Trp Asn Ala Thr Ser His His Thr Arg Pro Thr
20 25 30
Pro Gln Leu Pro Arg Gly Pro Asn
35 40

30

(2) INFORMATION FOR SEQ ID NO:276:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- 5 (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

Xaa Ser His Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val Phe Arg
1 5 10 15
Glu Leu Arg Asp Arg Trp Asn Ala Thr Ser His His Thr Arg Pro Thr
20 25 30
10 Pro Gln Leu Pro Arg Gly Pro Asn Ser
35 40

(2) INFORMATION FOR SEQ ID NO:277:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

15 (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

20 Xaa Ser Gln Gly Ser Lys Gln Cys Met Gln Tyr Arg Thr Gly Arg Leu
1 5 10 15
Thr Val Gly Ser Glu Tyr Gly Cys Gly Met Asn Pro Ala Arg His Ala
20 25 30
Thr Pro Ala Tyr Pro Ala Arg Leu Leu Pro Arg Tyr Arg
35 40 45

(2) INFORMATION FOR SEQ ID NO:278:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- 30 (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

Xaa Arg Val Gly Gln Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala
1 5 10 15
Arg Ser Cys Ala His Gln Gly Cys Gly Ala Gly Thr Arg Asn Ser His
20 25 30
Gly Cys Ile Thr Arg Pro Leu Arg Gln Ala Ser Ala His
35 40 45

5

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10 (ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=biotin-Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

Xaa Ser Gly Ser Gly Arg Val Gly Gln Cys Thr Asp Ser Asp Val Arg
1 5 10 15
Arg Pro Trp Ala Arg Ser Cys Ala
20

15

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

20

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

Xaa Arg Val Gly Gln Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala
1 5 10 15
Arg Ser Cys Ala
20

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

30

(D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

Xaa Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val
1 5 10 15
Asp Ser Asp Ser Asp Thr Asn Ala Lys His Ser Ser His Asn Arg Arg
20 25 30
Leu Arg Thr Arg Ser Arg Pro Asn Gly
35 40

10

(2) INFORMATION FOR SEQ ID NO:282:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

15

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

Xaa Arg Gly Ser Thr Gly Thr Ala Gly Gly Glu Arg Ser Gly Val Leu
1 5 10 15
20 Asn Leu His Thr Arg Asp Asn Ala Ser Gly Ser Gly Phe Lys Pro Trp
20 25 30
Tyr Pro Ser Asn Arg Gly His Lys
35 40

(2) INFORMATION FOR SEQ ID NO:283:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

Xaa Ser Gly Ser Gly Leu Tyr Ala Asn Pro Gly Met Tyr Ser Arg Leu
1 5 10 15
His Ser Pro Ala
20

(2) INFORMATION FOR SEQ ID NO:284:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
10 (D) OTHER INFORMATION: Xaa=biotin-Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

Xaa Ser Gly Ser Gly Leu Tyr Ala Asn Pro Gly Met Tyr Ser Arg Leu
1 5 10 15
His Ser Pro Ala
20

15 (2) INFORMATION FOR SEQ ID NO:285:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- 20 (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

Xaa Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys
1 5 10 15
Glu Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly Arg
20 25 30
Lys Val Phe Asn Arg Arg Arg Pro Ser Ala Ile Pro Thr
35 40 45

(2) INFORMATION FOR SEQ ID NO:286:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

Xaa Ser Pro Cys Gly Gly Ser Trp Gly Arg Phe Met Gln Gly Gly Leu
1 5 10 15
Phe Gly Gly Arg Thr Asp Gly Cys Gly Ala His Arg Asn Arg Thr Ser
20 25 30
Ala Ser Leu Glu Pro Pro Ser Ser Asp Tyr
35 40

(2) INFORMATION FOR SEQ ID NO:287:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

15 (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

Xaa Arg Tyr Lys His Asp Ile Gly Cys Asp Ala Gly Val Asp Lys Lys
1 5 10 15
Ser Ser Ser Val Arg Gly Gly Cys Gly Ala His Ser Ser Pro Pro Arg
20 25 30
20 Ala Gly Arg Gly Pro Arg Gly Thr Met Val Ser Arg Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:288:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

Xaa Ser Ala Arg Asp Ser Gly Pro Ala Glu Asp Gly Ser Arg Ala Val

1 5 10 15
Arg Leu Asn Gly Val Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg Ser
20 25 30
Asn Pro Arg Gly Arg Arg His Pro Gly Gly
35 40

(2) INFORMATION FOR SEQ ID NO:289:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other

10 (B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

Xaa Ser Lys Ser Gly Glu Gly Gly Asp Ser Ser Arg Gly Glu Thr Gly
1 5 10 15
Trp Ala Arg Val Arg Ser His Ala Met Thr Ala Gly Arg Phe Arg Trp
20 25 30
15 Tyr Asn Gln Leu Pro Ser Asp Arg
35 40

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

20 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

25 Xaa Ser Glu Ala Asn Leu Asp Gly Arg Lys Ser Arg Tyr Ser Ser Pro
1 5 10 15
Arg Arg Asn Ser Ser Thr Arg Pro Arg Thr Ser Pro Asn Ser Val His
20 25 30
Ala Arg Tyr Pro Ser Thr Asp His Asp
35 40

(2) INFORMATION FOR SEQ ID NO:291:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 258 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1 5 10 15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20 25 30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35 40 45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60
10 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65 70 75 80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85 90 95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100 105 110
Lys Asp Phe Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115 120 125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130 135 140
15 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145 150 155 160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165 170 175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180 185 190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195 200 205
Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
210 215 220
20 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Thr
225 230 235 240
Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp Ser Asp
245 250 255
Ser Asp

(2) INFORMATION FOR SEQ ID NO:236:

- (i) SEQUENCE CHARACTERISTICS:
25 (A) LENGTH: 259 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1 5 10 15
30 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20 25 30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
5 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
10 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Arg
 225 230 235 240
 Pro Tyr Ser Val Asp Ser Asp Ser Asp Thr Asn Ala Lys His Ser Ser
 245 250 255
15 His Asn Arg

(2) INFORMATION FOR SEQ ID NO:237:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 257 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

20 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
25 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
30 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 5 Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Thr Asn
 225 230 235 240
 Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg Ser Arg Pro
 245 250 255
 Asn

(2) INFORMATION FOR SEQ ID NO:238:

10

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 247 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

15

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 20 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 25 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Thr Asn
 225 230 235 240
 30 Ala Lys His Ser Ser His Asn
 245

(2) INFORMATION FOR SEQ ID NO:239:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 248 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

5 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1 5 10 15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20 25 30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35 40 45
10 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65 70 75 80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85 90 95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100 105 110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115 120 125
15 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130 135 140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145 150 155 160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165 170 175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180 185 190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195 200 205
20 Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
210 215 220
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Ser
225 230 235 240
His Asn Arg Arg Leu Arg Thr Arg
245

(2) INFORMATION FOR SEQ ID NO:240:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 248 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

25 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1 5 10 15
30 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20 25 30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
5 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
10 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Arg Arg
 225 230 235 240
 Leu Arg Thr Arg Ser Arg Pro Asn
 245

15

(2) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 282 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
25 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
30 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
5 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Arg Val
 225 230 235 240
 Gly Gln Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala Arg Ser Cys
 245 250 255
 Ala His Gln Gly Cys Gly Ala Gly Thr Arg Asn Ser His Gly Cys Ile
 260 265 270
 Thr Arg Pro Leu Arg Gln Ala Ser Ala His
 275 280

(2) INFORMATION FOR SEQ ID NO:242:

10

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 257 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

15

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60

20

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125

25

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp

30

145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Arg Val
 225 230 235 240
 Gly Gln Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala Arg Ser Cys
 245 250 255

Ala

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

5

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1 5 10 15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
10 20 25 30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35 40 45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65 70 75 80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85 90 95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
15 100 105 110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115 120 125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130 135 140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145 150 155 160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165 170 175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
20 180 185 190
20 195 200 205
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
210 215 220
Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
225 230 235 240
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Val Arg
245 250 255
Arg Pro Trp Ala Arg Ser Cys Ala His Gln Gly Cys Gly Ala Gly Thr
Arg Asn Ser

25

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

30

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
5 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
10 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
15 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Gly Thr
 225 230 235 240
 Arg Asn Ser His Gly Cys Ile Thr Arg Pro Leu Arg Gln Ala Ser Gln
 245 250 255
 His

(2) INFORMATION FOR SEQ ID NO:245:

20
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 282 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

25 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
30 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110

Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	
115						120						125				
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	
130						135					140					
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	
145						150				155			160			
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu	
						165				170			175			
5	Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr
						180				185			190			
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala	
195						200					205					
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg	
210						215					220					
Gly	Ser	Pro	Gly	Ile	Pro	Gly	Ser	Thr	Arg	Ala	Ala	Ala	Ser	Arg	Tyr	
225						230				235			240			
Lys	His	Asp	Ile	Gly	Cys	Asp	Ala	Gly	Val	Asp	Lys	Lys	Ser	Ser	Ser	
						245				250			255			
10	Val	Arg	Gly	Gly	Cys	Gly	Ala	His	Ser	Ser	Pro	Pro	Arg	Ala	Gly	Arg
						260				265			270			
Gly	Pro	Arg	Gly	Thr	Met	Val	Ser	Arg	Leu							
						275				280						

(2) INFORMATION FOR SEQ ID NO:246:

15	(i)	SEQUENCE CHARACTERISTICS:															
	(A)	LENGTH: 262 amino acids															
	(B)	TYPE: amino acid															
	(C)	STRANDEDNESS:															
	(D)	TOPOLOGY: unknown															
	(ii)	MOLECULE TYPE: peptide															
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:246:															
20	Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro	
	1					5			10			15					
	Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Glu	Tyr	Glu	Glu	His	Leu	
									20	25					30		
25	Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu	
								35	40			45					
	Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys	
						50				55		60					
	Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn	
						65				70		75			80		
	Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu	
						85				90			95				
30	Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser	
						100				105			110				
	Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	
						115				120			125				
	Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	
						130				135		140					
	Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	
						145				150		155			160		
	Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu	
						165				170			175				
	Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr	
						180				185			190				
30	Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala	
						195				200			205				

Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Arg Tyr
 225 230 235 240
 Lys His Asp Ile Gly Cys Asp Ala Gly Val Asp Lys Lys Ser Ser Ser
 245 250 255
 Val Arg Gly Gly Cys Gly
 260

5

(2) INFORMATION FOR SEQ ID NO:247:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 264 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 15 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 20 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 25 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Gly Cys
 225 230 235 240
 Asp Ala Gly Val Asp Lys Lys Ser Ser Ser Val Arg Gly Gly Cys Gly
 245 250 255
 Ala His Ser Ser Pro Pro Arg Ala
 260

(2) INFORMATION FOR SEQ ID NO:248:

- 30
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 259 amino acids
 - (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
5 1 5 10 15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20 25 30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35 40 45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65 70 75 80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
10 85 90 95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100 105 110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115 120 125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130 135 140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145 150 155 160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165 170 175
15 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180 185 190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195 200 205
Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
210 215 220
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Gly Ala
225 230 235 240
His Ser Ser Pro Pro Arg Ala Gly Arg Gly Pro Arg Gly Thr Met Val
245 250 255
20 Ser Arg Leu

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

25 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

Ser Gly Ser Pro Pro Cys Cys Ser Trp Gly Arg Phe Met Gln Gly
1 5 10 15
Gly Leu Phe Gly Gly Arg Thr Asp Gly Cys Gly Ala His Arg Asn Arg
20 25 30
30 Thr Ser Ala Ser Leu Glu Pro Pro Ser Ser Asp Tyr
35 40

(2) INFORMATION FOR SEQ ID NO:250:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

5 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

Ser His Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val Phe Arg Glu
1 5 10 15
Leu Arg Asp Arg Trp Asn Ala Thr Ser His His Thr Arg Pro Thr Pro
20 25 30
Gln Leu Pro Arg Gly Pro Asn Ser
35 40

10 (2) INFORMATION FOR SEQ ID NO:251:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

Asp Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg
1 5 10 15
Ser Arg Pro Asn Gly
20

(2) INFORMATION FOR SEQ ID NO:252:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

25 Cys Gly Ala Gly Thr Arg Asn Ser His Gly Cys Ile Thr Arg Pro Leu
1 5 10 15
Arg Gln Ala Ser Ala His Gly
20

(2) INFORMATION FOR SEQ ID NO:253:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

Xaa Thr Ala Ala Lys Asn Ser Ser His Asn Arg Arg Leu Arg Thr Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

10 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

Xaa Thr Asn Gly Lys Asn Ser Ser His Asn Arg Arg Leu Arg Thr Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:369:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

20 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

Xaa Thr Asn Ala Lys Ala Ser Ser His Asn Arg Arg Leu Arg Thr Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:370:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

30 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

Xaa Thr Asn Ala Lys His Ala Ser His Asn Arg Arg Leu Arg Thr Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:371:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

10

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

Xaa Thr Asn Ala Lys His Ser Ala His Asn Arg Arg Leu Arg Thr Arg
1 5 10 15

15

(2) INFORMATION FOR SEQ ID NO:372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

20

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

Xaa Thr Asn Ala Lys His Ser Ser Ala Asn Arg Arg Leu Arg Thr Arg
1 5 10 15

25

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

30

(A) NAME/KEY: Other

(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

Xaa Thr Asn Ala Lys His Ser Ser His Ala Arg Arg Leu Arg Thr Arg
1 5 10 15

5

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10 (ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

Xaa Thr Asn Ala Lys His Ser Ser His Asn Ala Arg Leu Arg Thr Arg
1 5 10 15

15

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

20 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

25 Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Ala Leu Arg Thr Arg
1 5 10 15

20

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

30 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

5 Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Ala Arg Thr Arg
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

10 (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

15 Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Ala Thr Arg
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

20 (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

25 Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Ala Arg
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

30 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

5 Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Ala
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

10

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

20

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

Xaa Lys Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr
1 5 10 15
Arg

(2) INFORMATION FOR SEQ ID NO:382:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
5 (D) OTHER INFORMATION: Xaa=Lys(dns)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg
1 5 10 15

- (2) INFORMATION FOR SEQ ID NO:383:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- 15 (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

Xaa Lys Ser Ser His Asn Arg Arg Leu Arg Thr Arg
1 5 10

- (2) INFORMATION FOR SEQ ID NO:384:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- 25 (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

Xaa Lys Ser Ser His Asn Arg Arg Leu Arg Thr Arg
1 5 10

- 30 (2) INFORMATION FOR SEQ ID NO:385:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- 5
- (A) NAME/KEY: Other
 - (B) LOCATION: 1...1
 - (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

Xaa Lys Thr Asn Ala Lys His Ser Ser His Asn Arg
1 5 10

10 (2) INFORMATION FOR SEQ ID NO:386:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- 15
- (A) NAME/KEY: Other
 - (B) LOCATION: 1...1
 - (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

Xaa Lys Thr Asn Ala Lys His Ser Ser His Asn Arg
1 5 10

20 (2) INFORMATION FOR SEQ ID NO:387:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- 25
- (A) NAME/KEY: Other
 - (B) LOCATION: 1...1
 - (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg
1 5 10 15

30 (2) INFORMATION FOR SEQ ID NO:388:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

5

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

Xaa Ala Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly
1 5 10 15

10

- (2) INFORMATION FOR SEQ ID NO:389:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

15

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

Xaa Pro Ala Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly
20 1 5 10 15

- (2) INFORMATION FOR SEQ ID NO:390:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

- 25 (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

30 Xaa Pro Gly Ala Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:391:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

5 (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

10 Xaa Pro Gly Asp Ala Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:392:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

15 (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

20 Xaa Pro Gly Asp Tyr Ala Cys Cys Gly Asn Gly Asn Ser Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:393:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

25 (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

30 Xaa Pro Gly Asp Tyr Asn Ala Cys Gly Asn Gly Asn Ser Thr Gly

1

5

10

15

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

5

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

Xaa Pro Gly Asp Tyr Asn Cys Ala Gly Asn Gly Asn Ser Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

15

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

Xaa Pro Gly Asp Tyr Asn Cys Cys Ala Asn Gly Asn Ser Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

25

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

Xaa Pro Gly Asp Tyr Asn Cys Cys Gly Ala Gly Asn Ser Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

Xaa Pro Gly Asp Tyr Asn Cys Cys Gly Asn Ala Asn Ser Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

Xaa Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Ala Ser Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

Xaa Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ala Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:400:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1

10 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

Xaa Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Ala Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:401:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1

20 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

Xaa Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:402:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

30 Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:403:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

5 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

Pro Gly Asp Tyr Asn Cys Cys Gly Asn Cys Asn Ser Thr Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:404:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

15 Ser Ala Arg Asp Ser Gly Pro Ala Glu Asp Gly Ser Arg Ala Val Arg
1 5 10 15
Leu Asn Gly Val Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg Ser Asn
20 25 30
Pro Arg Gly Arg Arg His Pro Gly
35 40

(2) INFORMATION FOR SEQ ID NO:405:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

Gly Thr Arg Asn Ser His Gly Cys Ile Thr Arg Pro Leu Arg Gln Ala
1 5 10 15
25 Ser Ala His

(2) INFORMATION FOR SEQ ID NO:406:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

30 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

5 Xaa Arg Val Gly Gln Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala
 1 5 10 15
Arg Ser Cys Ala His
 20

(2) INFORMATION FOR SEQ ID NO:407:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
10 (C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

15 (xii) SEQUENCE DESCRIPTION: SEQ ID NO:407:

Xaa Cys Gly Ala Gly Thr Arg Asn Ser His Gly Cys Ile Thr Arg Pro
 1 5 10 15
Leu Arg Gln Ala Ser Ala His
 20

20

25

30

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- 5
- (A) NAME/KEY: Other
 - (B) LOCATION: 1...1
 - (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

Xaa Arg Arg Leu Arg Thr Arg Ser Arg Pro Asn
1 5 10

10 (2) INFORMATION FOR SEQ ID NO:323:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- 15
- (A) NAME/KEY: Other
 - (B) LOCATION: 1...1
 - (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

Xaa Arg Arg Leu Arg Thr Arg Ser Arg
1 5

20 (2) INFORMATION FOR SEQ ID NO:324:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
25 (ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

Xaa Arg Arg Leu Arg Thr Arg
1 5

30 (2) INFORMATION FOR SEQ ID NO:325:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

5

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

Xaa Arg Arg Leu Arg Thr Arg Ser Arg Pro Asn
1 5 10

10

- (2) INFORMATION FOR SEQ ID NO:326:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

15

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

Xaa Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys
1 5 10 15
Glu Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly
20 25

20

- (2) INFORMATION FOR SEQ ID NO:327:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

25

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

30

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

Xaa Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly Arg Lys

1 5 10 15
Val Phe Asn Arg Arg Arg Pro Ser Ala Ile Pro Thr
20 25

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

Xaa Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys
1 5 10 15
Glu Pro Gly Cys
20

(2) INFORMATION FOR SEQ ID NO:329:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

20

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

Xaa Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly
1 5 10

25

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

30

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

Xaa Arg Lys Val Phe Asn Arg Arg Arg Pro Ser Ala Ile Pro Thr
1 5 10 15

5 (2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

10 (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

Xaa Arg Lys Val Phe Asn Arg Arg Arg Pro Ser
1 5 10

15 (2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

20 (ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

Xaa Asn Arg Arg Arg Pro Ser Ala Ile Pro Thr
1 5 10

25 (2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

30 (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys (dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

Xaa Asn Arg Arg Arg Pro Ser
5 1 5

(2) INFORMATION FOR SEQ ID NO:334:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

10 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp
1 5 10 15
Ser Asp Ser Asp Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu
20 25 30
Arg Thr Arg Ser Arg Pro Asn Gly
35 40

15 (2) INFORMATION FOR SEQ ID NO:335:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys Glu
1 5 10 15
Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly Arg Lys
20 25 30
Val Phe Asn Arg Arg Arg Pro Ser Ala Ile Pro Thr
35 40

25 (2) INFORMATION FOR SEQ ID NO:336:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

30 (A) NAME/KEY: Other
(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

Xaa Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys
1 5 10 15
Glu Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr
5 20 25 30

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

10 (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

15 Xaa Asn Leu Arg Ser Asp Asn Ala Lys Glu Pro Gly Asp Tyr Asn Cys
1 5 10 15
Cys Gly Asn Gly Asn Ser Thr Gly Arg Lys Val Phe Asn Arg
20 25 30

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

20 (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

Xaa Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly Arg
1 5 10 15
Lys Val Phe Asn Arg Arg Pro Ser Ala Ile Pro Thr
20 25

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: Other
(B) LOCATION: 1...1
5 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

Xaa Ala Ser His Asn Arg Arg Leu Arg Thr Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:340:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

15 (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

Xaa Ser Ala His Asn Arg Arg Leu Arg Thr Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:341:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

25 (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

Xaa Ser Ser Ala Asn Arg Arg Leu Arg Thr Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:342:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- 5
- (A) NAME/KEY: Other
 - (B) LOCATION: 1...1
 - (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

Xaa Ser Ser His Ala Arg Arg Leu Arg Thr Arg
1 5 10

10 (2) INFORMATION FOR SEQ ID NO:343:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- 15
- (A) NAME/KEY: Other
 - (B) LOCATION: 1...1
 - (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

Xaa Ser Ser His Asn Ala Arg Leu Arg Thr Arg
1 5 10

20 (2) INFORMATION FOR SEQ ID NO:344:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- 25
- (A) NAME/KEY: Other
 - (B) LOCATION: 1...1
 - (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

Xaa Ser Ser His Asn Arg Ala Leu Arg Thr Arg
1 5 10

30 (2) INFORMATION FOR SEQ ID NO:345:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

5

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

Xaa Ser Ser His Asn Arg Arg Ala Arg Thr Arg
1 5 10

10

(2) INFORMATION FOR SEQ ID NO:346:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

15

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

Xaa Ser Ser His Asn Arg Arg Leu Ala Thr Arg
20 1 5 10

20

(2) INFORMATION FOR SEQ ID NO:347:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

25 (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

30 Xaa Ser Ser His Asn Arg Arg Leu Arg Ala Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:348:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

5 (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

10 Xaa Ser Ser His Asn Arg Arg Leu Arg Thr Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:349:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

15 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

Ser Ser His Asn Arg Arg Leu Arg Thr Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:350:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

25 (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

Xaa Gly Arg Asn His Asp Val Val Ser Ser Asn Thr His Lys Ser Tyr
1 5 10 15
Arg Ser Pro Arg Ser Ala Ser Tyr Pro Arg Leu Ser Asn Asp Arg Thr
20 25 30
30 Asp Arg Thr Glu Pro Ala Pro Ser Ser
35 40

(2) INFORMATION FOR SEQ ID NO:351:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

5 (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

10 Xaa Arg Asn Thr Arg Asn Lys Thr Ser Arg Leu Ser Ala Asn Pro His
1 5 10 15
Arg Ser His Arg
20

(2) INFORMATION FOR SEQ ID NO:352:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

15 (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 20...20
(D) OTHER INFORMATION: Xaa=Lys(dns)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg Ser
1 5 10 15
Arg Pro Asn Xaa
20

(2) INFORMATION FOR SEQ ID NO:353:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

30 (A) NAME/KEY: Other
(B) LOCATION: 10...10
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

Arg Arg Leu Arg Thr Arg Ser Arg Lys Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1

10 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

Xaa Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys
1 5 10 15
Glu Pro Gly Asp Tyr
20

15 (2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

20 (A) NAME/KEY: Other
(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

Xaa Ser Asp Asn Ala Lys Glu Pro Gly Asp Tyr Asn Cys Cys Gly Asn
1 5 10 15
Gly Asn Ser Thr Gly
20

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

30 (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

5 Xaa Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:357:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

10 (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

15 Xaa Glu Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:358:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

20 (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

25 Xaa Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:359:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

30 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

5 Xaa Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly
 1 5 10

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

10

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: MEMORY
 (B) STRAIN: DISPLAY MEMORY

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

Xaa Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:361:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

25

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

Xaa Lys Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly Arg Arg His
1 5 10 15
Pro Gly

30

(2) INFORMATION FOR SEQ ID NO:362:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

5

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

Xaa Lys Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly Arg Arg His
1 5 10 15

10 Pro Gly

- (2) INFORMATION FOR SEQ ID NO:363:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

15

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

20 Xaa Lys Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr
1 5 10 15
Arg

- (2) INFORMATION FOR SEQ ID NO:364:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

25

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

30

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

Xaa Thr Asn Ala Lys His Ser Ser Cys Asn Arg Arg Cys Arg Thr Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other

- (B) LOCATION: 1...1

- (D) OTHER INFORMATION: Xaa=Lys(dns)

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

Xaa Thr Asn Ala Lys His Ser Ser Cys Asn Arg Arg Leu Arg Cys Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other

- (B) LOCATION: 1...1

- (D) OTHER INFORMATION: Xaa=Lys(dns)

15 20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

Xaa Ala Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other

- (B) LOCATION: 1...1

- (D) OTHER INFORMATION: Xaa=Lys(dns)

25 30

(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: Modified Base
(B) LOCATION: 1...1
5 (D) OTHER INFORMATION: Xaa=biotin-S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

Xaa Gly Ser Gly Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro
1 5 10 15
Tyr Ser Val Asp Ser Asp Ser Asp Thr Asn Ala Lys His Ser Ser His
20 25 30
Asn Arg Arg Leu Arg Thr Arg Ser Arg Pro Asn Gly
35 40

10

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

15

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

20 Xaa Arg Val Gly Gln Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala
1 5 10 15
Arg Ser Cys Ala His Gln Gly
20

25

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

Xaa Cys Gly Ala Gly Thr Arg Asn Ser His Gly Cys Ile Thr Arg Pro
1 5 10 15
Leu Arg Gln Ala Ser Ala His Gly
20

(2) INFORMATION FOR SEQ ID NO:294:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
10 (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

Xaa Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly
1 5 10 15
Arg Arg His Pro Gly
20

15 (2) INFORMATION FOR SEQ ID NO:295:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
20 (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

Xaa Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly
1 5 10

25 (2) INFORMATION FOR SEQ ID NO:296:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
30 (A) NAME/KEY: Other

- (B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

Xaa Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly
1 5 10 15

5

(2) INFORMATION FOR SEQ ID NO:297:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
10 (ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

Xaa Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly Arg Arg His Pro
1 5 10 15
Gly

15

(2) INFORMATION FOR SEQ ID NO:298:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

20

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg
1 5 10 15
Ser Arg Pro Asn
20

(2) INFORMATION FOR SEQ ID NO:299:

30

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:300:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: Other
(B) LOCATION: 1...1
15 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

Xaa Ser Ser His Asn Arg Arg Leu Arg Thr Arg Ser Arg Pro Asn
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:301:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: Other
25 (B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

Xaa Ser Ser His Asn Arg Arg Leu Arg Thr Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:302:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- 5
- (A) NAME/KEY: Other
 - (B) LOCATION: 1...1
 - (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

Xaa Val Arg Arg Pro Trp Ala Arg Ser Cys Ala His Gln Gly Cys Gly
1 5 10 15
Ala Gly Thr Arg Asn Ser
20

10 (2) INFORMATION FOR SEQ ID NO:303:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None
15 (ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

Xaa Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala Arg Ser Cys
1 5 10 15

20 (2) INFORMATION FOR SEQ ID NO:304:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 41 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

25 (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

30 Xaa Ser Arg Ala Asn Thr Asp Gly Arg Lys Ser Arg Tyr Ser Ser Pro
1 5 10 15
Arg Arg Asn Ser Ser Thr Glu Pro Arg Leu Ser Pro Asn Ser Val His

	20		25		30
Ala Arg Tyr Pro Ser Thr Asp His Asp					
	35		40		

(2) INFORMATION FOR SEQ ID NO:305:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: Other
 - (B) LOCATION: 1...1
 - (D) OTHER INFORMATION: Xaa=Lys(dns)

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

Xaa	Glu	Asn	Ala	Asn	Thr	Arg	Lys	Ser	Ser	Arg
1				5					10	

(2) INFORMATION FOR SEQ ID NO:306:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: Other
 - (B) LOCATION: 1...1
 - (D) OTHER INFORMATION: Yes, I would like to see the sequence.

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

Xaa	Ser	Asn	Pro	Arg	Gly	Arg	Arg	His	Pro	Gly
1				5					10	

(2) INFORMATION FOR SEQ ID NO:307:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys (dns)

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

Xaa Glu Asn Ala Asn Thr
1 5

(2) INFORMATION FOR SEQ ID NO:308:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- 10 (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

Xaa Ala Asn Thr Arg Lys Ser
1 5

(2) INFORMATION FOR SEQ ID NO:309:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- 20 (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

Xaa Thr Arg Lys Ser Ser
1 5

(2) INFORMATION FOR SEQ ID NO:310:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- 30 (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

Xaa Arg Lys Ser Ser Arg
1 5

(2) INFORMATION FOR SEQ ID NO:311:

5

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

10

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

Xaa Lys Ser Ser Arg Ser Asn
1 5

15

(2) INFORMATION FOR SEQ ID NO:312:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

20

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

Xaa Ser Ser Arg Ser Asn Pro Gly
1 5

25

(2) INFORMATION FOR SEQ ID NO:313:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

30

(ix) FEATURE:

- (A) NAME/KEY: Other

(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

Xaa Arg Ser Asn Pro Arg Gly
1 5

5

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10 (ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

Xaa Ser Asn Pro Arg Gly
1 5

15

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

20 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

Xaa Pro Arg Gly Arg Arg His
1 5

25

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

30 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys (dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

5 Xaa Arg Arg His Pro Gly
 1 5

(2) INFORMATION FOR SEQ ID NO:317:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

10 (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys (dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

15 Xaa Lys Ser Ser Arg Gly Asn
 1 5

(2) INFORMATION FOR SEQ ID NO:318:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

20 (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys (dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

25 Xaa Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro Gly
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:319:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

30 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

5 Xaa Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly Arg Arg His Pro
 1 5 10 15
 Gly

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

Xaa Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly Arg Arg His Pro
1 5 10 15
Gly

(2) INFORMATION FOR SEQ ID NO:321:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

25

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

Xaa Thr Asn Ala Lys His Ser Ser His Asn
1 5 10

30

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS: